

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation	..
pir2:S16848	+	579.00	880.71	4.2e-41	136	Ig lambda chain	V-I region precursor
pir2:S25758	+	559.00	846.73	1.9e-39	235	Ig lambda chain	human
pir2:S14675	+	557.00	823.04	2.8e-39	235	Ig lambda chain	human
pir2:S25759	+	544.00	824.71	3.5e-38	235	Ig lambda chain	human
pir2:S04519	+	528.00	804.52	8.6e-37	118	Ig lambda chain	precursor V-II
pir2:S44105	+	490.50	748.15	1.2e-33	112	Ig lambda chain	V-J region - human
pir2:S19671	+	478.00	729.30	1.4e-32	111	Ig lambda chain	V-I region (clone)
pir2:S51149	+	473.50	722.55	3.4e-32	110	antibody light chain	V region - human
pir2:S46396	+	470.00	717.19	6.7e-32	111	Ig lambda chain	V region - human
pir2:S31515	+	469.50	716.38	7.9e-32	112	Ig lambda chain	V region - human
pir2:S36281	+	468.00	714.17	9.8e-32	111	Ig lambda chain	V region - human
pir2:S44123	+	466.50	711.84	1.3e-31	112	Ig lambda chain	V-J region - human
pir1:L2HUMC	+	461.00	703.58	3.8e-31	111	Ig lambda chain	V-I region (Mc)
pir1:L2HUNG	+	460.50	702.76	4.2e-31	112	Ig lambda chain	V-I region (Ni)
pir2:S46395	+	460.50	702.76	4.2e-31	112	Ig lambda chain	V region - human
pir2:S27412	+	460.00	702.13	4.6e-31	110	Ig lambda chain	V-J region - human
pir1:L2HUPR	+	460.00	702.07	4.6e-31	111	Ig lambda chain	V-I region (Tr)
pir2:S36057	+	458.00	699.82	6.9e-31	99	Ig lambda chain	human (fragment)
pir2:S38497	+	458.00	699.04	6.8e-31	111	Ig lambda chain	human (fragment)
pir2:S36056	+	457.00	698.31	8.4e-31	99	Ig lambda chain	human (fragment)
pir2:S46397	+	457.00	697.53	8.3e-31	111	Ig lambda chain	V region (VL-16)
pir1:L2HUNI	+	456.00	696.01	1.0e-30	111	Ig lambda chain	V-I region (Ne)
pir2:S36256	+	454.00	692.99	1.5e-30	111	Ig lambda chain	V region (clone)
pir1:L2HUVL	+	453.00	691.48	1.8e-30	111	Ig lambda chain	V-I region (Vi)
pir2:S57442	+	448.00	683.97	4.8e-30	110	Ig lambda chain	V-I region - human
pir1:L2HUBH	+	443.00	676.35	1.3e-29	111	Ig lambda chain	V-I region - human
pir2:S36053	+	439.00	671.07	2.8e-29	99	Ig lambda chain	V-I region (Bc)
pir1:L2HUBS	+	439.00	670.42	2.7e-29	109	Ig lambda chain	human (fragment)
pir1:L2HUBO	+	437.00	667.27	4.0e-29	111	Ig lambda chain	V-I region (Bu)
pir1:L2HUBG	+	437.00	667.27	4.0e-29	111	Ig lambda chain	V-I region (Bc)
pir1:L2HUBV	+	436.00	665.76	4.9e-29	111	Ig lambda chain	V-I region (Tc)
pir1:L2HUVN	+	435.00	664.25	5.9e-29	111	Ig lambda chain	V-I region (Wi)
pir2:S19673	+	429.00	655.17	1.9e-28	111	Ig lambda chain	V-I region (clone)
pir2:S38499	+	426.00	650.63	3.4e-28	111	Ig lambda chain	V region (clone)
pir2:S36058	+	425.00	649.90	4.2e-28	99	Ig lambda chain	human (fragment)
pir2:S25746	+	423.50	641.72	5.0e-28	236	Ig lambda chain	human
pir2:S09712	+	414.00	631.40	3.4e-27	130	Ig lambda chain	V region - human
pir2:S05270	+	412.00	624.35	4.7e-27	130	Ig lambda chain	precursor V-J
pir2:S78057	+	411.00	626.86	6.1e-27	130	Ig lambda chain	precursor V-I
pir2:S78058	+	409.00	623.89	9.0e-27	129	Ig lambda chain	precursor V-J
pir2:S25752	+	407.00	616.85	1.2e-26	233	Ig lambda chain	human

C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25758  
R:Combiato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda  
A:Reference number: S16439; MUID:91257162  
A:Accession: S25758  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-235 <COM>  
A:Cross-references: EMBL:X57823; NID:g33745; PIDN:CAA40960.1; PID:g33746  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:150-218/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 559.00 Length: 130  
Ratio: 4.620 Gaps: 0  
Percent Similarity: 93.077 Percent Identity: 81.538

alignment\_block:  
US-09-019-441-1 x S25758 ..

Align seg 1/1 to: S25758 from: 1 to: 235

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1 ATGGCTGGACTGCTGCTCCGTCACCTCCTCAGGCGACAGGATC 50
|||||.....|.....|.....|.....|.....|.....|
1 MetAlaTrpAlaLeuPheLeuThrLeuLeuThrGlnGlyThrGlyLe 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCCTCTGTCTGGGCTCCTG 100
|||||.....|.....|.....|.....|.....|.....|
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerPro 34
101 GACAGTGGTCCACCATCTCTGCACTGGACCGGACGATGAGTGGTGT 150
|||||.....|.....|.....|.....|.....|.....|
34 yGlnSerIleThrIleSerCysThrGlySerSerAspValGlyGly 50
151 TATAACTATGCTCTCTGGTACCAACACACCCAGGCAAGCCCAAACT 200
|||||.....|.....|.....|.....|.....|.....|
51 TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLys 67
201 CATGATTATGATGCTCCTAAGCGGGCTCAGGGGTCTCTGATGCTTCT 250
|||||.....|.....|.....|.....|.....|.....|
67 uMetIleTyrAspValThrAsnArgProSerGlyValSerAsnArgPhe 84
251 CTGGCTCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 300
|||||.....|.....|.....|.....|.....|.....|
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAGTAG 350
|||||.....|.....|.....|.....|.....|.....|
101 ProGluAspGluAlaAspTyrTyrCysThrSerLysThrSerSerSerPh 117
351 TTCTGTTATTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 390
|||||.....|.....|.....|.....|.....|.....|
117 eTyrValPheGlyThrGlyThrLysValSerValLeuGly 130
```

seq\_name: pir2:S14675

seq\_documentation\_block:  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 19-May-1994 #text\_change 21-Jan-2000  
C:Accession: S14675; S12445  
R:Vasicek, T.J.  
submitted to the EMBL Data Library, February 1990  
A:Reference number: S14675  
A:Accession: S14675  
A:Molecule type: DNA  
A:Residues: 1-235 <VASI>  
A:Cross-references: EMBL:X51754

R:Vasicek, T.J.; Leder, P.  
J. Exp. Med. 172, 609-620, 1990  
A:Title: Structure and expression of the human immunoglobulin lambda genes.  
A:Reference number: S12440; MUID:90324881  
A:Accession: S12445  
A:Molecule type: DNA  
A:Residues: 1-129 <VAS2>  
A:Cross-references: EMBL:X51754  
C:Genetics:  
A:Introns: 16/1; 130/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:150-218/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 557.00 Length: 130  
Ratio: 4.528 Gaps: 0  
Percent Similarity: 94.615 Percent Identity: 80.000

alignment\_block:  
US-09-019-441-1 x S14675 ..

Align seg 1/1 to: S14675 from: 1 to: 235

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1 ATGGCTGGACTGCTGCTCCGTCACCTCCTCAGGCGACAGGATC 50
|||||.....|.....|.....|.....|.....|.....|
1 MetAlaTrpAlaLeuLeuIleLeuThrLeuLeuThrGlnGlyThrGlyLe 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCCTCTGTCTGGGCTCCTG 100
|||||.....|.....|.....|.....|.....|.....|
17 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeu 34
101 GACAGTGGTCCACCATCTCTGCACTGGACCGGACGATGAGTGGTGT 150
|||||.....|.....|.....|.....|.....|.....|
34 yGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 50
151 TATAACTATGCTCTCTGGTACCAACACACCCAGGCAAGCCCAAACT 200
|||||.....|.....|.....|.....|.....|.....|
51 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLys 67
201 CATGATTATGATGCTCCTAAGCGGGCTCAGGGGTCTCTGATGCTTCT 250
|||||.....|.....|.....|.....|.....|.....|
67 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPhe 84
251 CTGGCTCCAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCC 300
|||||.....|.....|.....|.....|.....|.....|
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 100
301 GCTGAGGACGAGGCTGATTATTACTGTTGTTTCATATACAAACAGTAG 350
|||||.....|.....|.....|.....|.....|.....|
101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrAlaGlySerAsn 117
351 TTCTGTTATTCGGAAGAGGAGCCCGGTTGACCGTCTAGGT 390
|||||.....|.....|.....|.....|.....|.....|
117 rLeuIlePheGlyGlyGlyThrArgLeuThrValLeuGly 130
```

seq\_name: pir2:S25759

seq\_documentation\_block:  
Ig lambda chain - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S25759  
R:Combiato, G.; Klobbeck, H.G.  
Eur. J. Immunol. 21, 1513-1522, 1991  
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin  
A:Reference number: S16439; MUID:91257162  
A:Accession: S25759  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-235 <COM>  
A:Cross-references: EMBL:X57824; NID:g33747; PIDN:CAA40961.1; PID:g33748

C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:150-218/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 544.00 Length: 130  
Ratio: 4.496 Gaps: 0  
Percent Similarity: 93.077 Percent Identity: 78.462

alignment\_block:

US-09-019-441-1 x S25759 ..

Align seg 1/1 to: S25759 from: 1 to: 235

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1 ATGGCCTGGACTCTGCTCCTCGTCACCTCTCTCAGGCGCAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetAlatrprThrLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlyse 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 CTGGGCTCAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGGTCCTCG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GACAGTCGGTCACCATCTCTGCTGCACTGGAAACAGCATGAGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 TATAACTATGTCTCTCTGTGTACCAACACACAGCCAGGAAAGCCCCAACT 200
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 CATGATTATGATCTGCTAAGCGGCTCAGGGTCTCTGTCATCGCTCT 250
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 uMetIlePheValSerGlyArgProSerGlyIleSerArgPheS 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 CTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 GCTGAGGACGAGCTGATTATTACTGTGTTCATATACAAACAGTAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerTh 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TTTGTTATTCGGAAGAGGAGCCCGTTCCAGCTCTAGGT 390
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 rValValPheGlyGlyGlyThrSerValThrValLeuGly 130
```

seq\_name: pir2:S04519

seq\_documentation\_block:

Ig lambda chain precursor V-II region (2.1) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 21-Jan-2000  
C:Accession: S04519  
R:Brookly, F.; Alexandre, D.; Chuchana, P.; Huck, S.; Lefranc, M.P.  
Nucleic Acids Res. 17, 3976, 1989  
A:Title: First nucleotide sequence of a human immunoglobulin variable lambda gene belong  
A:Reference number: S04519; MUID:89282402  
A:Accession: S04519  
A:Molecule type: DNA  
A:Residues: 1-118 <BRO>  
A:Cross-references: EMBL:X14616; NID:g33749; PIDN:CAA32770.1; PID:g736248  
C:Genetics:  
A:Introns: 16/1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-118/Product: Ig lambda chain V-II region #status predicted <MAT>  
F:34-111/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 528.00 Length: 118

Ratio: 4.757 Gaps: 0  
Percent Similarity: 94.068 Percent Identity: 85.593

alignment\_block:

US-09-019-441-1 x S04519 ..

Align seg 1/1 to: S04519 from: 1 to: 118

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1 ATGGCCTGGACTCTGCTCCTCGTCACCTCTCTCAGGCGCAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetAlatrprAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlyse 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 CTGGGCTCAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGGTCCTCG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GACAGTCGGTCACCATCTCTGCTGCACTGGAAACAGCATGAGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlySer 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 TATAACTATGTCTCTGTGTACCAACACACAGCCAGGAAAGCCCCAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 TyrAsnLeuValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 CATGATTATGATCTGCTAAGCGGCTCAGGGTCTCTGTCATCGCTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 uMetIleTyrGluGlySerLysArgProSerGlyValSerAsnArgPheS 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 CTGGCTCCAACTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 GCTGAGGACGAGCTGATTATTACTGTGTTCATATACAAACAGTAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlySerSerTh 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TTTG 354
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 rLeu 118
```

seq\_name: pir2:S44105

seq\_documentation\_block:

Ig lambda chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44105  
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variabl  
A:Reference number: S44105  
A:Accession: S44105  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-112 <HAW>  
A:Cross-references: EMBL:X31388; NID:g472959; PIDN:CAA83263.1; PID:g940517  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-92/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 490.50 Length: 112  
Ratio: 4.671 Gaps: 1  
Percent Similarity: 93.750 Percent Identity: 84.821

alignment\_block:

US-09-019-441-1 x S44105 ..

Align seg 1/1 to: S44105 from: 1 to: 112

```
58 CAGTCTGCCCGACTCAGCTCCCTCTGTGTCTGGGTCCTCTGGACAGTC 107
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

370 ACCCGGTTGACCGTCCTAGGT 390





## alignment\_block:

US-09-019-441-1 x S36281 ..

Align seg 1/1 to: S36281 from: 1 to: 111

```
58 CAGTCTGCCCCGACTACGCTCCCTCTGTCTGGGTCTCCTGGACAGTC 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17
108 GGTCAACATCTCTGCACTGGAACACGAGTGGTGGTTATTAAC 157
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsn 34
158 ATGTCTCTCTGTACACACACACACACGAGCAAGCCCAAACTCATGAT 207
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 yValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLeuLeuIle 50
208 TATGATGTGCTAAGCGGCTCAGGGTCTCTGATCGCTTCTTGCTC 257
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 TyrGluValSerLysArgProSerGlyValSerAsnArgPheSerGlySe 67
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAG 307
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGlu 84
308 ACGAGGCTGATTATTACTGTGTTCATATACACACAGTAGCAGCTTGT 357
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 sPGluAlaAspTyrPheCysSerAlaTyrAlaProThrGlyIleMetMet 100
358 TTCGGAGAGAGGACCGGTTGACCGTCTAGGT 390
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111
```

## seq\_name: pir2:S44123

## seq\_documentation\_block:

Ig lambda chain V-J region - human  
C:Species: Homo sapiens (man)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 24-May-2001  
C:Accession: S44123  
R:Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.  
submitted to the EMBL Data Library, March 1994  
A:Description: Idiotype vaccination against human B-cell lymphoma: rescue of variable H  
A:Reference number: S44105  
A:Accession: S44123  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-112 <HAW>  
A:Cross-references: EMBL:231382; NID:g472977; PIDN:CAA83257.1; PID:g940534  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-92/Domain: immunoglobulin homology <IMM>

## alignment\_scores:

Quality: 466.50 Length: 112  
Ratio: 4.574 Gaps: 1  
Percent Similarity: 91.071 Percent Identity: 82.143

## alignment\_block:

US-09-019-441-1 x S44123 ..

Align seg 1/1 to: S44123 from: 1 to: 112

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58 CAGTCTGCCCCGACTACGCTCCCTCTGTCTGGGTCTCCTGGACAGTC 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17
108 GGTCAACATCTCTGCACTGGAACACGAGTGGTGGTTATTAAC 157
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsn 34
```

```
158 ATGTCTCTCTGTACACACACACACGAGCAAGCCCAAACTCATGAT 207
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 euGlySerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50
208 TATGATGTGCTAAGCGGCTCAGGGTCTCTGATCGCTTCTTGCTC 257
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 TyrGluGlySerLysArgProSerGlyValSerAsnArgPheSerGlySe 67
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAG 307
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGlu 84
308 ACGAGGCTGATTATTACTGTGTTCATATACACACAGTAGCAGT...TTG 354
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
84 sPGluAlaAspTyrTyrCysCysSerTyrAlaGlySerSerThrSerTip 100
355 TTATTCGGAAGAGGACCGGTTGACCGTCTAGGT 390
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 ValPheGlyGlyGlyThrLysLeuThrValLeuGly 112
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## seq\_name: pir1:L2HUMC

## seq\_documentation\_block:

Ig lambda chain V-II region (Mcg) - human  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 24-Nov-1999  
C:Accession: A90381; A01975  
R:Pett, J.W.; Deutsch, H.F.  
Biochemistry 13, 4102-4114, 1974  
A:Title: Primary structure of the Mcg lambda chain.  
A:Reference number: A90381; MUID:75013804  
A:Accession: A90381  
A:Molecule type: protein  
A:Residues: 1-111 <PET>  
A>Note: the C region of this chain has the Kern+ and Mcg+ markers  
R:Pett, J.W.; Deutsch, H.F.  
Immunohemistry 12, 643-652, 1975  
A:Title: A new lambda-chain gene.  
A:Reference number: A91745; MUID:76093781  
A:Contents: annotation; lambda chain genes  
A:Note: the Mcg-type C region appears to be correlated with a very unusual V-region s  
R:Edmundson, A.B.; Ely, K.R.; Abola, E.E.; Schiffer, M.; Panagiotopoulos, N.  
Biochemistry 14, 3953-3961, 1975  
A:Title: Rotational allomerism and divergent evolution of domains in immunoglobulin 1  
A:Reference number: A90391  
A:Contents: annotation; X-ray crystallography, 2.3 angstroms  
C:Comment: This is a Bence Jones protein.  
C:Genetics:  
A:Gene: GDB:IGLV6  
A:Cross-references: GDB:119342; OMIM:147240  
A:Map position: 22q11.2-22q11.2  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( C  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer  
F:15-92/Domain: immunoglobulin homology <IMM>  
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #st  
F:22-50/Disulfide bonds: #status predicted

## alignment\_scores:

Quality: 461.00 Length: 111  
Ratio: 4.564 Gaps: 0  
Percent Similarity: 90.991 Percent Identity: 79.279

## alignment\_block:

US-09-019-441-1 x L2HUMC ..

Align seg 1/1 to: L2HUMC from: 1 to: 111

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58 CAGTCTGCCCCGACTACGCTCCCTCTGTCTGGGTCTCCTGGACAGTC 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 GlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuGlyGlnSe 17
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108 GGTCAACATCTCTGCACTGGACACCGAGTACGTTGGTGGTATAACT 157
||||| 17 rValThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnT 34
||||| 158 ATGTCTCTCTGGTACCAACACACCGAGGAAAGCCCAAACTCATGATT 207
||||| 34 yrValSerTrpTyrGlnGlnHisAlaGlyLysAlaProLysValIle 50
||||| 208 TATGATGTCGCTAAGCGGGCTCAGGGGTCCTCGATGCTCTCTGGCTC 257
||||| 51 TyrGluValAlaAsnLysArgProSerGlyValProAspArgPheSerGly 67
258 CAAGTCTGGCAACACCGCTCCCTGACCATCTCTGGCTCCAGGCTGAGG 307
||||| 67 rLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGlnAlaGluA 84
||||| 308 ACGAGGCTGATTATTACTGTGTGTTATACAAACAGTAGCATTGTTTA 357
||||| 84 spGluAlaAspTyrTyrCysSerSerTyrGluGlySerAspAsnPheVal 100
358 TTCGGAAGAGGGACCGGTTGACCGTCTAGGT 390
||||| 101 PheGlyThrGlyThrLysValThrValLeuGly 111

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seq\_name: pir1:L2HUNG

seq\_documentation\_block:  
 Ig lambda chain V-II region (Nig-84) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 04-Dec-1986 #sequence\_revision 04-Dec-1986 #text\_change 02-Sep-1997  
 C:Accession: A01971  
 R:Tonokike, H.; Kametani, F.; Hoshi, A.; Shinoda, T.; Isobe, T.  
 FEBS Lett. 185, 139-141, 1985  
 A:Title: Amino acid sequence of an amyloidogenic Bence Jones protein in myeloma-associated  
 A:Reference number: A01971; MUID:85204383  
 A:Accession: A01971  
 A:Molecule type: protein  
 A:Residues: 1-112 <TON>  
 A:Comment: This is a Bence Jones protein isolated from an individual with myeloma-associated  
 C:Genetics:  
 A:Gene: GDB:IGLV6  
 A:Cross-references: GDB:119342; OMIM:147240  
 A:Map position: 22q11.2-22q11.2  
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: amyloid; heterotetramer; immunoglobulin  
 F:15-92/Domain: immunoglobulin homology <IMM>  
 F:22-90/Disulfide bonds: #status predicted

alignment\_scores:  
 Quality: 460.50 Length: 112  
 Ratio: 4.471 Gaps: 1  
 Percent Similarity: 91.964 Percent Identity: 78.571  
 alignment\_block:  
 US-09-019-441-1 x L2HUNG ..  
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58 CAGTCTGCCCGGACTAGCCTCCCTCTGTCTGTGGGTCTCTGGACAGTC 107
||||| 1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17
108 GGTCAACATCTCTGCACTGGACACCGAGTACGTTGGTGGTATAACT 157
||||| 17 rIleThrIleSerCysThrGlyThrSerAspValGlyGlyTyrAsp 34
158 ATGTCTCTCTGGTACCAACACCGAGGAAAGCCCAAACTCATGATT 207
||||| 34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuLeu 50

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208 TATGATGTCGCTAAGCGGGCTCAGGGGTCCTGTGATCGCTTCTCTGGCTC 257
||||| 51 TyrAspValAlaSerArgProSerGlyIleSerAsnArgPheSerGlySe 67
258 CAAGTCTGGCAACACCGCTCCCTGACCATCTCTGGCTCCAGGCTGAGG 307
||||| 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84
||||| 308 ACGAGGCTGATTATTACTGTGTGTTATAT...ACAACCACTAGCATTG 354
||||| 84 spGluAlaAspTyrTyrCysSerSerPheThrThrAsnSerArgAla 100
355 TTATTTCGGAAGAGGGACCGGTTGACCGTCTAGGT 390
||||| 101 ValPheGlyGlyGlyThrLysLeuSerValLeuGly 112

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seq\_name: pir2:S46395

seq\_documentation\_block:  
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 C:Species: Homo sapiens (man)  
 C:Date: 27-Jan-1995 #sequence\_revision 27-Jan-1995 #text\_change 20-Jun-2000  
 C:Accession: S46395  
 R:Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.  
 J. Mol. Biol. 239, 68-78, 1994  
 A:Title: In vitro assembly of repertoires of antibody chains on the surface of phage  
 A:Reference number: S46390; MUID:94254092  
 A:Accession: S46395  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-112 <FIG>  
 A:Cross-references: EMBL:Z31583; NID:g509791; PIDN:CAA83488.1; PID:g1335167  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:15-92/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
 Quality: 460.50 Length: 112  
 Ratio: 4.471 Gaps: 1  
 Percent Similarity: 91.964 Percent Identity: 81.250  
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 US-09-019-441-1 x S46395 ..  
 Align seg 1/1 to: S46395 from: 1 to: 112

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58 CAGTCTGCCCGGACTAGCCTCCCTCTGTCTGTGGGTCTCTGGACAGTC 107
||||| 1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17
108 GGTCAACATCTCTGCACTGGACACCGAGTACGTTGGTGGTATAACT 157
||||| 17 rIleThrIleSerCysThrGlyThrSerSerAspValGlySerTyrLysL 34
158 ATGTCTCTCTGGTACCAACACCGAGGAAAGCCCAAACTCATGATT 207
||||| 34 euValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetile 50
208 TATGATGTCGCTAAGCGGGCTCAGGGGTCCTGTGATCGCTTCTCTGGCTC 257
||||| 51 TyrGluValSerAsnArgProSerGlyValSerAsnArgPheSerGlySe 67
258 CAAGTCTGGCAACACCGCTCCCTCTGACCATCTCTGGGCTCCAGGCTGAGG 307
||||| 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84
308 ACGAGGCTGATTATTACTGTGTGTTATATACAACTAGCATTG... 354
||||| 84 spGluAlaGlyTyrTyrCysSerSerTyrThrSerSerThrValArg 100
355 TTATTTCGGAAGAGGGACCGGTTGACCGTCTAGGT 390

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||||| |||||:|||||||  
101 serPheGlyGlyThrLysLeuThrValLeuGly 112

OM of: US-09-019-441-1 to: SwissProt\_40.\* out\_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-Q/cgn2\_1/uspo1\_spo1/us09019441/runat\_23092002\_095259\_6394/app\_query.fasta\_1.1860  
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-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000  
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-GAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
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Search information block:

Query: US-09-019-441-1  
Query length: 390  
Database: SwissProt\_40.\*  
Database sequences: 105224  
Database length: 38719550  
Search time (sec): 62.410000

score\_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
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SwissProt_40:LV2K_HUMAN	+	460.50	791.38	2.0e-36	112 ! P04209 homo sapiens (human)
SwissProt_40:LV2D_HUMAN	+	460.00	790.60	2.2e-36	111 ! P01707 homo sapiens (human)
SwissProt_40:LV2B_HUMAN	+	456.00	783.73	5.3e-36	111 ! P01705 homo sapiens (human)
SwissProt_40:LV2H_HUMAN	+	453.00	778.58	1.0e-35	111 ! P01711 homo sapiens (human)
SwissProt_40:LV2C_HUMAN	+	443.00	761.41	9.3e-35	111 ! P01706 homo sapiens (human)
SwissProt_40:LV2E_HUMAN	+	439.00	754.69	2.2e-34	109 ! P01708 homo sapiens (human)
SwissProt_40:LV2G_HUMAN	+	437.00	751.10	3.5e-34	111 ! P01710 homo sapiens (human)
SwissProt_40:LV2A_HUMAN	+	436.00	749.39	4.3e-34	111 ! P01704 homo sapiens (human)
SwissProt_40:LV2I_HUMAN	+	435.00	747.67	5.4e-34	111 ! P01712 homo sapiens (human)
SwissProt_40:LV1G_HUMAN	+	401.00	687.97	9.7e-31	130 ! P06316 homo sapiens (human)
SwissProt_40:LV2J_HUMAN	+	387.50	666.19	1.9e-29	110 ! P01713 homo sapiens (human)
SwissProt_40:LV2F_HUMAN	+	359.00	617.18	1.0e-26	111 ! P01702 homo sapiens (human)
SwissProt_40:LV2L_HUMAN	+	357.00	613.74	1.6e-26	111 ! P80422 homo sapiens (human)
SwissProt_40:LV6E_HUMAN	+	355.50	609.78	2.2e-26	131 ! P06319 homo sapiens (human)
SwissProt_40:LV1B_HUMAN	+	345.50	593.92	2.0e-25	112 ! P01700 homo sapiens (human)
SwissProt_40:LV1A_HUMAN	+	345.00	593.14	2.2e-25	111 ! P01699 homo sapiens (human)
SwissProt_40:LV1C_HUMAN	+	344.00	591.42	2.7e-25	111 ! P01701 homo sapiens (human)
SwissProt_40:LV1F_HUMAN	+	342.00	588.14	4.2e-25	112 ! P04208 homo sapiens (human)
SwissProt_40:LV1H_HUMAN	+	331.50	569.88	4.3e-24	111 ! P06887 homo sapiens (human)
SwissProt_40:LV6D_HUMAN	+	327.00	562.23	2.8e-23	111 ! P06317 homo sapiens (human)
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SwissProt_40:LV6A_HUMAN	+	319.50	549.28	6.0e-23	112 ! P01721 homo sapiens (human)
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SwissProt_40:LV4A_HUMAN	+	312.00	536.86	3.1e-22	106 ! P01715 homo sapiens (human)
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SwissProt_40:LV4C_HUMAN	+	289.00	497.29	4.9e-20	107 ! P01717 homo sapiens (human)
SwissProt_40:LV4D_HUMAN	+	286.00	492.22	9.6e-20	106 ! P01718 homo sapiens (human)
SwissProt_40:LV3B_HUMAN	+	283.00	486.68	1.9e-19	111 ! P80748 homo sapiens (human)
SwissProt_40:LV5A_HUMAN	+	279.00	480.05	4.5e-19	108 ! P01719 homo sapiens (human)
SwissProt_40:LV7A_HUMAN	+	264.00	454.06	1.2e-17	111 ! P01720 homo sapiens (human)
SwissProt_40:LV1B_MOUSE	+	257.50	441.64	5.2e-17	129 ! P01724 mus musculus (mouse)
SwissProt_40:LV1D_MOUSE	+	255.50	438.20	8.0e-17	129 ! P01726 mus musculus (mouse)
SwissProt_40:LV0A_HUMAN	+	253.50	435.59	1.2e-16	117 ! P04211 homo sapiens (human)
SwissProt_40:KV1W_HUMAN	+	252.50	433.05	1.6e-16	129 ! P04431 homo sapiens (human)

SwissProt_40:LV1E_MOUSE	+	252.50	433.05	1.6e-16	129 ! P01727 mus musculus (mouse)
SwissProt_40:KV4B_HUMAN	+	252.00	431.94	1.7e-16	133 ! P06313 homo sapiens (human)
SwissProt_40:KV07_RABIT	+	248.00	426.82	4.1e-16	108 ! P01688 oryctolagus cuniculus
SwissProt_40:KV6K_MOUSE	+	246.00	423.38	6.4e-16	108 ! P04945 mus musculus (mouse)
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seq\_name: SwissProt\_40:LV2F\_HUMAN

seq\_documentation\_block:

ID	LV2F_HUMAN	STANDARD;	PRT;	111 AA.
AC	P01709;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	13-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig lambda chain V-II region MGC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE.			
RX	MEDLINE=75013804; PubMed=4415202;			
RT	Fett J.W., Deutsch H.F.;			
RT	"Primary structure of the Mcg lambda chain.";			
RL	Biochemistry 13:4102-4114(1974).			
RN	[2]			
RP	LAMBDA CHAIN GENES.			
RX	MEDLINE=76093781; PubMed=812801;			
RT	Fett J.W., Deutsch H.F.;			
RT	"A new lambda-chain gene.";			
RL	Immunochimistry 12:643-652(1975).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).			
RA	Edmundson A.B., Ely K.R., Abola E.E., Schiffer M.,			
RA	Panagiotopoulos N.;			
RT	"Rotational allomerism and divergent evolution of domains in			
RT	immunoglobulin light chains.";			
RL	Biochemistry 14:3953-3961(1975).			
RN	[4]			
RP	X-RAY CRYSTALLOGRAPHY.			
RX	MEDLINE=90133913; PubMed=2515285;			
RT	Ely K.R., Herron J.N., Harker M., Edmundson A.B.;			
RT	"Three-dimensional structure of a light chain dimer crystallized in			
RT	water. Conformational flexibility of a molecule in two crystal			
RT	forms.";			
RL	J. Mol. Biol. 210:601-615(1989).			
CC	-!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.			
CC	-!- MISCELLANEOUS: THE MCG-TYPE C REGION APPEARS TO BE CORRELATED WITH			
CC	A VERY UNUSUAL V-REGION SUBSTITUTION, 103-THR ABOVE FOR GLY,			
CC	SUGGESTING THAT THE V-C JOINING MECHANISM IS NOT ALWAYS RANDOM.			
CC	-!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+			
CC	MARKERS.			
CC	PIR; A01975; L2HUMC.			
DR	PDB; 2MCG; 15-JUL-92.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	InterPro: IPR003596; Ig_V.			
DR	Pfam; PF00047; Ig; 1.			
DR	SMART; SM00406; IG; 1.			
KW	Immunoglobulin V region; Bence-Jones protein; 3D-structure.			
FT	MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.			
FT	DISULFID 22 90 BY SIMILARITY.			
FT	STRAND 5 5			
FT	STRAND 10 12			
FT	STRAND 18 23			
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 Percent Similarity: 90.991 Percent Identity: 79.279

alignment\_block:  
 US-09-019-441-1 x LV2F\_HUMAN ..

Align seg 1/1 to: LV2F\_HUMAN from: 1 to: 111

58 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTC 107  
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 1 GlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuGlyGlnSe 17  
 108 GGTCAACATCTCTGCACTGGAACACCGATGAGCTGGTGGTTATAACT 157  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
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 158 ATGTCTCTGTTACCAACACACACCGAGCAAGCCCAAACTCATGATT 207  
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 208 TATGATCGCTAAGCGGCTCAGGGCTCTGAGGTCTCTGATCGCTCTGGCTC 257  
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 258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGCTCCAGGCTCAGG 307  
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 67 rLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGlnAlaGlu 84  
 308 ACGAGGCTGATTATTACTGTGTTTCATATACACAGCTAGCATTGTGTTA 357  
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 84 spGluAlaAspTyrTyrCysSerSerTyrGluGlySerAspAsnPheVal 100  
 358 TTCGGAAGAGGCGCGGTGACCGTCTAGGT 390  
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 101 PheGlyThrGlyThrLysValThrValLeuGly 111

seq\_name: SwissProt\_40:LV2K\_HUMAN

seq\_documentation\_block:  
 ID LV2K\_HUMAN STANDARD; PRT; 112 AA.

AC P04209;  
 DT 20-MAR-1987 (Rel. 04, Created)  
 DT 20-MAR-1987 (Rel. 04, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-II region NIG-84.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85204383; PubMed=3922791;  
 RA Tonolike H., Kametani F., Hoshi A., Shinoda T., Isobe T.;  
 RT "Amino acid sequence of an amyloidogenic Bence Jones protein in  
 RT myeloma-associated systemic amyloidosis.";  
 RL FEBS Lett. 185:139-141(1985).  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN ISOLATED FROM AN  
 CC INDIVIDUAL WITH MYELOMA-ASSOCIATED SYSTEMIC AMYLOIDOSIS.  
 DR PIR; A01971; L2HUNG.  
 DR HSSP; P01709; 2MCG.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.

DR SMART; SM00406; Ig; 1.  
 KW Immunoglobulin V region; Amyloid; Bence-Jones protein.  
 FT DISULFID 22 90 BY SIMILARITY.  
 FT NON\_TER 112 112  
 SQ SEQUENCE 112 AA; 11581 MW; 988FEF363AE1E4F3 CRC64;

alignment\_scores:  
 Quality: 460.50 Length: 112  
 Ratio: 4.471 Gaps: 1  
 Percent Similarity: 91.964 Percent Identity: 78.571

alignment\_block:

US-09-019-441-1 x LV2K\_HUMAN ..

Align seg 1/1 to: LV2K\_HUMAN from: 1 to: 112

58 CAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCTGGGTCTCTCTGGACAGTC 107  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17  
 108 GGTCAACATCTCTGCACTGGAACACCGATGAGCTGGTGGTTATAACT 157  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 17 rIleThrIleSerCysThrGlyThrSerAspValGlyGlyTyrAsp 34  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 158 ATGTCTCTGTTACCAACACACCGAGCAAGCCCAAACTCATGATT 207  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuIle 50  
 208 TATGATCGCTAAGCGGCTCAGGGCTCTGAGGTCTCTGATCGCTCTGGCTC 257  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 51 TyrAspValAsnSerArgProSerGlyIleSerAsnArgPheSerGlySe 67  
 258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGCTCCAGGCTCAGG 307  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGlu 84  
 308 ACGAGGCTGATTATTACTGTGTTTCATAT...ACAACAGCTAGCATTGTTG 354  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 84 spGluAlaAspTyrTyrCysSerSerPheThrThrAsnSerArgAla 100  
 355 TTATTCGGAAGAGGCGCGGTGACCGTCTAGGT 390  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 101 ValPheGlyGlyThrLysLeuSerValLeuGly 112

seq\_name: SwissProt\_40:LV2D\_HUMAN

seq\_documentation\_block:  
 ID LV2D\_HUMAN STANDARD; PRT; 111 AA.

AC P01707;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig lambda chain V-II region TRO.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=80114123; PubMed=118915;  
 RA Scholz R., Yang C., Hilschmann N.;  
 RT "Rule of antibody structure. Primary structure of a human monoclonal  
 RT IgA1-immunoglobulin (myeloma protein Tro). VI. Amino acid sequence of  
 RT the L-chain, lambda-type, subgroup II.";  
 RL Hoppe-Sevler's Z. Physiol. Chem. 360:1903-1918(1979).  
 CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 CC PIR; A01973; L2HUTR.  
 DR HSSP; P01709; 2MCG.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Ig; 1.

KW Immunoglobulin V region.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12E8F6E1 CRC64;

alignment\_scores:  
Quality: 460.00 Length: 111  
Ratio: 4.510 Gaps: 0  
Percent Similarity: 91.892 Percent Identity: 79.279

alignment\_block:  
US-09-019-441-1 x LV2D\_HUMAN ..

Align seg 1/1 to: LV2D\_HUMAN from: 1 to: 111

58 CAGTCTGCCGCGACTCAGCTCCCTCTGTGTCTGGTCTCTCTGGACAGTC 107  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
1 GlnSerAlaLeuThrGlnProArgSerValSerGlySerProGlyGlnSe 17  
108 GGTCAACATCTCTGCACCTGGAACACCGGATGACGTTGGTGGTTATAACT 157  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
17 rValThrIleSerCysThrGlyThrSerSerAspValGlyAlaTyrAsnS 34  
158 ATGCTCTCTGTACCAACACACCGCAGCAGCAAGCCCAACTCATGATT 207  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
34 ervAlSerTrpTyrGlnHisProGlyLysAlaProLysLeuMetile 50  
208 TATGATCGCTAAGCGGCGCTCAGGGCTCTCTGATCGCTCTCTGGCTC 257  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
51 PheAspValThrLysArgProSerGlyValProAspArgLeuSerGlySe 67  
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGCTCAGG 307  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
67 rLysSerGlyAspThrAlaSerLeuThrIleSerGlyLeuArgAlaAspA 84  
308 ACGAGGCTGATTATTACTGTGTTCATATACACACGATAGCATTGTGTA 357  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
84 spGluAlaAspTyrTyrCysSerTyrAlaGlyArgTyrSerValile 100  
358 TTCGGAAGAGGACCGGCTTACCGCTCTAGGT 390  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
101 PheGlyGlyThrLysLeuThrValLeuGly 111

seq\_name: SwissProt\_40:LV2B\_HUMAN

seq\_documentation\_block:  
ID LV2B\_HUMAN STANDARD; PRT; 111 AA.  
AC P01705;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region NEI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=72233223; PubMed=5043326;  
RA Garver F.A., Hilschmann N.;  
RT "The primary structure of a monoclonal human lambda-type  
immunoglobulin L-chain of subgroup II (Bence-Jones protein NEI).";  
RL Eur. J. Biochem. 26:10-32(1972).  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01970; L2HUNI.  
DR HSSP; P01709; 2MCG.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; Glycoprotein.

FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT CARBOHYD 96 96 N-LINKED (GLCNAC. .).  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11591 MW; AD6D156584D087EB CRC64;

alignment\_scores:  
Quality: 456.00 Length: 110  
Ratio: 4.471 Gaps: 0  
Percent Similarity: 92.727 Percent Identity: 79.091

alignment\_block:  
US-09-019-441-1 x LV2B\_HUMAN ..

Align seg 1/1 to: LV2B\_HUMAN from: 1 to: 111

58 CAGTCTGCCGCGACTCAGCTCCCTCTGTGTCTGGTCTCTCTGGACAGTC 107  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17  
108 GGTCAACATCTCTGCACCTGGAACACCGGATGACGTTGGTGGTTATAACT 157  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
17 rIleThrIleSerCysThrGlyThrSerSerAspValGlySerTyrAsnP 34  
158 ATGCTCTCTGTACCAACACACCGCAGCAGCAAGCCCAACTCATGATT 207  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
34 heValSerTrpTyrGlnAsnProGlyLysAlaProLysLeuMetile 50  
208 TATGATCGCTAAGCGGCGCTCAGGGCTCTCTGATCGCTCTCTGGCTC 257  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
51 TyrGluGlyAsnLysArgProSerGlyValSerAsnArgPheSerGlySe 67  
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGCTCAGG 307  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
67 rLysSerGlyLysThrAlaSerLeuThrIleSerGlyLeuGlnValGluA 84  
308 ACGAGGCTGATTATTACTGTGTTCATATACACACGATAGCATTGTGTA 357  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
84 spGluAlaAspTyrTyrCysSerTyrAlaGlyAsnSerThrArgVal 100  
358 TTCGGAAGAGGACCGGCTTACCGCTCTAGGT 387  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
101 PheGlyGlyThrArgValThrValLeu 110

seq\_name: SwissProt\_40:LV2H\_HUMAN

seq\_documentation\_block:  
ID LV2H\_HUMAN STANDARD; PRT; 111 AA.  
AC P01711;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region VII.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71215142; PubMed=5087637;  
RA Ponstingl H., Hilschmann N.;  
RT "Structural rule of antibodies. Complete primary structure of a  
monoclonal immunoglobulin L chain of the lambda type, subgroup II  
(Bence Jones protein VII).";  
RL Hoppe-Seyler's Z. Physiol. Chem. 352:859-877(1971).  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01977; L2HUVL.  
DR HSSP; P01709; 2MCG.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.

```
FT DISULFID      22      90      BY SIMILARITY.
FT NON_TER      111      111
SQ SEQUENCE      111 AA; 11445 MW; 3913736B3EF367E0 CRC64;
```

## alignment\_scores:

Quality: 453.00 Length: 110  
Ratio: 4.485 Gaps: 0  
Percent Similarity: 91.818 Percent Identity: 79.091

## alignment\_block:

US-09-019-441-1 x LV2H\_HUMAN ..

Align seg 1/1 to: LV2H\_HUMAN from: 1 to: 111

```
61 TCTCCCGGAGTCCCTCTGCTGCTGGGTCCTCTGGACAGTCGGT 110
||||| ||||||| ||||||| ||||||| ||||||| |||||||
2 SerAlaLeuThrGlnProAlaSerValSerGlySerLeuGlnSerI 18
111 CACCATCTCTGCACTGGAACACCGATGACGTTGGTGTATAACTATG 160
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
18 eThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnTyrV 35
161 TCTCTGGTACCAACACACCGAGGCAAGCCCAAACTCATGATTAT 210
|||||:|||||:|||||:|||||:|||||:|||||:|||||
35 aISerTrpPheGlnGlnHisProGlyThrAlaProLysLeuIleSer 51
211 GATGTCGCTAAGCGGCGCTCAGGGGCTCTGATCGCTCTCTGGCTCAA 260
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
52 GluValArgAsnArgProSerGlyValSerAspArgPheSerGlySerLy 68
261 GTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACG 310
|||||:|||||:|||||:|||||:|||||:|||||:|||||
68 sSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAspG 85
311 AGCTGATTATTACTGTGTTTCATATACACACAGTAGCAGCTTTGTTATC 360
|||||:|||||:|||||:|||||:|||||:|||||:|||||
85 luAlaAspTyrTyrCysSerSerTyrThrSerSerAsnSerValPhe 101
361 GGAAGAGGAGCGCGGTTGACCGCTCCTAGGT 390
||||| ||||||| ||||||| ||||||| ||||||| |||||||
102 GlyGlyGlyThrLysLeuThrValLeuGly 111
```

seq\_name: SwissProt\_40:LV2C\_HUMAN

seq\_documentation\_block:

ID LV2C\_HUMAN STANDARD; PRT; 111 AA.  
AC P01706;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region BOH.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=75115478; PubMed=804002;  
RA Kohler H., Rudofsky S., Kluskens L.;  
RT "The primary structure of a human lambda II chain.";  
RL J. Immunol. 114:415-421(1975).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE O2+ MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01972; L2HUBH.  
DR HSSP; P01709; 2MCG.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region.  
MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.

```
FT DISULFID      22      90      BY SIMILARITY.
FT NON_TER      111      111
SQ SEQUENCE      111 AA; 11650 MW; 94520309932623E8 CRC64;
```

## alignment\_scores:

Quality: 443.00 Length: 111  
Ratio: 4.567 Gaps: 0  
Percent Similarity: 87.387 Percent Identity: 79.279

## alignment\_block:

US-09-019-441-1 x LV2C\_HUMAN ..

Align seg 1/1 to: LV2C\_HUMAN from: 1 to: 111

```
58 CACTGCTGCCCGGAGTCCCTCTGCTGCTGGGTCCTCTGGACAGTC 107
||||| ||||||| ||||||| ||||||| ||||||| |||||||
1 GluSerAlaLeuThrGlnProArgSerValSerGlySerProGlyGlnSe 17
108 GGTCAACCATCTCTGCACTGGAACACCGATGACGTTGGTGTATAACT 157
||||| ||||||| ||||||| ||||||| ||||||| |||||||
17 rValThrIleSerCysAlaGlyThrSerSerAspValGlyGlyAsnHisP 34
158 ATGTCCTCTGGTACCAACACACCGAGGCAAGCCCAAACTCATGATT 207
:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 heValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuIle 50
208 TATGATGTCGCTAAGCGGCGCTCAGGGGCTCTGATCGCTCTCTGGCTC 257
||||| ||||||| ||||||| ||||||| ||||||| |||||||
51 TyrGlyValAsnLysArgProSerGlyValProTyrArgPheSerGlySe 67
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84
308 ACAGGCTGATTATTACTGTGTTTCATATACACACAGTAGCAGCTTTGTTA 357
||||| ||||||| ||||||| ||||||| ||||||| |||||||
84 spGluAlaHisTyrTyrCysSerTyrAlaGlyArgPheThrTrpVal 100
358 TTCGGAAGAGGAGCGCGGTTGACCGCTCCTAGGT 390
||||| ||||||| ||||||| ||||||| ||||||| |||||||
101 PheGlyGlyGlyThrAsnLeuThrValLeuGly 111
```

seq\_name: SwissProt\_40:LV2E\_HUMAN

seq\_documentation\_block:

ID LV2E\_HUMAN STANDARD; PRT; 109 AA.  
AC P01708;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region BUR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=80006606; PubMed=113407;  
RA Infante A.J., Putnam F.W.;  
RT "Primary structure of a human IgA1 immunoglobulin. V. Amino acid  
sequence of a human IgA lambda light chain (Bur).";  
RL J. Biol. Chem. 254:9006-9016(1979).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR; A01974; L2HUBR.  
DR HSSP; P01709; 2MCG.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region.





FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.  
FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11713 MW; FD20AEF4CE5364E2 CRC64;

alignment\_scores:  
Quality: 436.00 Length: 110  
Ratio: 4.360 Gaps: 0  
Percent Similarity: 90.909 Percent Identity: 74.545

alignment\_block:

US-09-019-441-1 x LV2A\_HUMAN ..

Align seg 1/1 to: LV2A\_HUMAN from: 1 to: 111

58 CAGTCTCCCGGACTCAGCCTCCCTCTGTCTGGGTCTCTCGACAGTC 107  
|||||  
1 GlnSerAlaLeuThrGlnProAlaSerValSerAlaSerProGlyGlnSe 17  
|||||  
108 GGTCCACCATCTCTGCACTGGAACACGAGCATGACGTTGGTGTATAACT 157  
|||||  
17 rIleThrIleSerCysThrGlyThrThrAsnAspIleGlySerTyrSert 34  
|||||  
158 ATGTCTCTGGTACCAACACACAGCCAGGAAAGCCGCCAACATCATGATT 207  
|||||  
34 yValSerTyrGlnGlnTyrProGlyLysAlaProLysValLeulle 50  
|||||  
208 TATGATCTCGCTAAGCGGGCTCAGGGGTCTCTGATCGTCTCTGGCTC 257  
|||||  
51 PheAspValAsnSerArgProSerGlyValSerHisArgPheSerGlyse 67  
|||||  
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGCGCTGAGG 307  
|||||  
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84  
|||||  
308 ACAGGCTGATTATTACTGTGTTTCATATACACAGCAGTACCATTTGTTA 357  
|||||  
84 spGluAlaHisTyrPheCysSerSerTyrArgThrSerGlyThrIle 100  
|||||  
358 TTCGGAAGAGGAGCCCGTTGACCGTCTA 387  
|||||  
101 PheGlyGlyGlyThrTyrValThrValLeu 110  
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seq\_name: SwissProt\_40:LV2I\_HUMAN

seq\_documentation\_block:

ID LV2I\_HUMAN STANDARD; PRT; 111 AA.  
AC P01712;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-II region WIN.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79062503; PubMed=102365;  
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;  
RT "Amino acid sequence of the human myeloma lambda chain Win.";  
RL Biochim. Biophys. Acta 537:9-21(1978).  
CC -!- MISCELLANEOUS: THIS IS A BENICE-JONES PROTEIN.  
DR PIR: A01978; L2HUN.  
DR HSSP: P01709; 2MCG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig\_1.  
DR SMART: SM00406; IGV; 1.  
KW Immunoglobulin V region; Benice-Jones protein.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT DISULFID 22 90 BY SIMILARITY.

FT NON\_TER 111 111  
SQ SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

alignment\_scores:  
Quality: 435.00 Length: 111  
Ratio: 4.439 Gaps: 0  
Percent Similarity: 88.288 Percent Identity: 76.577

alignment\_block:

US-09-019-441-1 x LV2I\_HUMAN ..

Align seg 1/1 to: LV2I\_HUMAN from: 1 to: 111

58 CAGTCTCCCGGACTCAGCCTCCCTCTGTCTGGGTCTCTCGACAGTC 107  
|||||  
1 GlnSerAlaLeuThrGlnProArgValSerGlySerProGlyGlnSe 17  
|||||  
108 GGTCCACCATCTCTGCACTGGAACACGAGCATGACGTTGGTGTATAACT 157  
|||||  
17 rValThrIleSerCysThrGlySerTyrSerAsnValThrGlyTyrAsnH 34  
|||||  
158 ATCTCTCTCGTACCAACACACGAGGAAAGCCGCCAACATCATGATT 207  
|||||  
34 iValSerTyrGlnGlnAspProGlyLysValProLysLeuMetile 50  
|||||  
208 TATGATCTCGCTAAGCGGGCTCAGGGGTCTCTGATCGTCTCTGGCTC 257  
|||||  
51 TyrAspValAspLysArgProSerGlyValProAspArgPheSerGlyse 67  
|||||  
258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGCGCTGAGG 307  
|||||  
67 rLysSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaAsnA 84  
|||||  
308 ACCAGCTGATTATTACTGTGTTTCATATACACAGTACCATTTGTTA 357  
|||||  
84 snGluAlaAspTyrTyrCysSerSerTyrGlyGlyThrTyrSerLeulle 100  
|||||  
358 TTCGGAAGAGGAGCCCGTTGACCGTCTAGGT 390  
|||||  
101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111  
|||||

seq\_name: SwissProt\_40:LV1G\_HUMAN

seq\_documentation\_block:

ID LV1G\_HUMAN STANDARD; PRT; 130 AA.  
AC P06316;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig lambda chain V-I region BL2 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85062823; PubMed=6095199;  
RA Tsujimoto Y., Croce C.M.;  
RT "Molecular cloning of a human immunoglobulin lambda chain variable  
sequence.";  
RL Nucleic Acids Res. 12:8407-8414(1984).  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
DR EMBL: X01147; CAA25598.1; -.  
DR PIR: A01966; LIHUBL.

seq_documentation_block:	
AC	LV2J_HUMAN
ID	STANDARD;
IC	PRT;
AD	110 AA.
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig lambda chain V-II region NIG-58.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE.
RX	MEDLINE=81215386; PubMed=6787031;

seq_documentation_block:		
ID	LVID_HUMAN	STANDARD; PRT; 111 AA.
AC	P01702;	
DT	21-JUL-1986 (Rel. 01, Created)	
DT	21-JUL-1986 (Rel. 01, Last sequence update)	
DT	13-JUL-1999 (Rel. 38, Last annotation update)	
DE	Ig lambda chain V-I region NIG-64.	
OS	homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
OX	NCBI_TaxID=9606;	
	[1]	
RN	SEQUENCE.	
RP		
RX	MEDLINE=83186114; PubMed=6404900;	
RA	Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,	

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RA Shimizu A.;
RT "Comparative studies on the structure of the light chains of human
RL Immunoglobulins. IV. Assignment of a subgroup.",
DR J. Biochem. 93:421-429(1983).
DR PIR; A01965; LIHUNG.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 89
FT NON_TER 111 111 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

alignment_scores:
  Quality: 359.00 Length: 112
  Ratio: 3.740 Gaps: 2
Percent Similarity: 85.714 Percent Identity: 64.286

alignment_block:
US-09-019-441-1 x LV1D_HUMAN ..
Align seg 1/1 to: LV1D_HUMAN from: 1 to: 111

58 CAGTCTGCCCGACTCAGCTCCCTCTGTGCTCTCTGGTCTCTGGACAGTC 107
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||
1 GlnSerValLeuThrGlnProProSerValSerAlaAlaProGlyGlnGI 17

108 GGTCCACCATCTCTGCTGCTGGAACACGATGAGTGGTGGTTATAACT 157
:|||||:  ||||||:  ||||||:  ||||||:  ||||||:  ||||||:  |||
17 uValThrIleSerCysSerGlySerSerSerAsnIleGlyAsp...Asp 33

158 ATGTCTCTGGTACCAACACACCCAGGCAAGCCCAACTCATGATT 207
:|||||:  ||||||:  ||||||:  ||||||:  ||||||:  ||||||:  |||
33 heValSerTrpTyrGlnGlnLeuProGlyThrAlaProLysLeuLeuIle 49

208 TATGATCTGCTAAGCGGGCTCTCAGGGCTCTCTGATCGCTCTCTGGCTC 257
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
50 TyrAspAsnAsnLysArgProSerGlyIleProAspArgPheSerGlySe 66

258 CAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
66 rLysSerGlyThrSerAlaThrLeuGlyIleThrGlyLeuGlnThrGlyA 83

308 ACAGAGCTGATTATTACTGTGTTCATATACACCACT...AGCACTTG 354
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
83 sPGluAlaAspTyrTyrCysGlyThrTrpAspSerSerLeuSerValGly 99

355 TTATTCGAAGAGGAGCGGTTGACCGTCTCTAGGT 390
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
100 MetPheGlyGlyGlyThrArgValThrValLeuGly 111

seq_name: SwissProt_40:LV2L_HUMAN

seq_documentation_block:
ID LV2L_HUMAN STANDARD; PRT; 111 AA.
AC P80422;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma lambda chain V-II region DOT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal

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RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 90
FT NON_TER 111 111 BY SIMILARITY.
SQ SEQUENCE 111 AA; 11787 MW; F358B1EA2CD7109A CRC64;

alignment_scores:
  Quality: 357.00 Length: 110
  Ratio: 4.011 Gaps: 0
Percent Similarity: 80.909 Percent Identity: 63.636

alignment_block:
US-09-019-441-1 x LV2L_HUMAN ..
Align seg 1/1 to: LV2L_HUMAN from: 1 to: 111

61 TCTGCCCGACTCAGCTCCCTCTGTGCTCTCTGGTCTCTGGACAGTCGT 110
|||||  |||||||  |||  |||||||  |||||||  |||||||  |||
2 SerAlaLeuThrGlnProArgSerLeuSerGlySerProGlyGlnAlaVa 18

111 CACCATCTCTGCTGCTGNAACCGATGAGTGGTGGTTATAACTATG 160
|||||  |||||||  ||||||  |||  |||  |||  |||  |||  |||
18 lThrIleSerCysThrGlyLeuProSerValValAspAspAsnPheV 35

161 TCTCTGTGTACCAACACGCGCAAGCCCAACTCATGATTAT 210
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
35 alSerTrpTyrGlnGlnThrProGlyArgAlaProArgLeuLeuIleTyr 51

211 GATGCTCCTAAGCGGGCTCTCAGGGCTCTCTGATCGCTCTCTGGCTCAA 260
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||
52 AspAspSerLeuArgProSerGlyValProAsnArgPheSerGlySerLy 68

261 GTCTGGCAACACGCGCTCTGACCATCTCTGGGCTCCAGGCTCAGGACG 310
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
68 sSerAspThrLysAlaAlaLeuThrIleSerGlyLeuGlnProAspAspG 85

311 AGGCTGATTATTACTGTGTTCATATACACCACTAGTCTCTGTTATTC 360
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||
85 luAlaThrTyrPheCysCysSerTyrValGlyAsnTyrIlePheValPhe 101

361 GGAAGAGGAGCGGTTGACCGTCTCTAGGT 390
|||||  ||||||  ||||||  ||||||  ||||||  ||||||  |||
102 GlyGlnGlyThrAspLeuThrValLeuGly 111

seq_name: SwissProt_40:LV6E_HUMAN

seq_documentation_block:
ID LV6E_HUMAN STANDARD; PRT; 131 AA.
AC P06319;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-VI region EB4 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85215660; PubMed=3923440;
RA Anderson M.L.M., Brown L., McKenzie E., Kellow J.E., Young B.D.;
RT "Cloning and sequence analysis of an Ig lambda light chain mRNA
expressed in the Burkitt's lymphoma cell line EB4.";
RL Nucleic Acids Res. 13:2931-2941(1985).
DR PIR; A01990; L6HUEB.
DR HSSP; P01709; 2MCG.

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Align seg 1/1 to: LVGE_HUMAN from: 1 to: 131

1  ATGGCCTGGAGCTCTGTCTCCCTCGTCACACCTCTCACTCAGGGCACAGGATC 50
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1  MetAlaTrpAlaProLeuLeuThrLeuLeuAlaHisCysThrAspCyl 17
   ::::::::::::::::::::::::::::::::::::::::::::
51  CTGGGCTCAGTCTGCCCGGACTCAGCCTCCTCTGTGTCTGGGTCTCCCTG 100
   :::::::::: ::::::::::::::::::::::::::::::::::::
17  strPALAAsnPhenMetLeuThrGlnProHisSerValSerGluSerProG 34
   :::::::::: ::::::::::::::::::::::::::::::::::::::
101  GACAGTCGGCTCACCATCTCCTGCACTGGAAACCACCGCATGACTGGTGGT 150
   ::::::::::::::::::::::::::::::::::::::::::::::
34  lyLysThrValThrIleSerCysThrGlyAsnSerGlySerIleAlaSer 50
   ::::::::::::::::::::::::::::::::::::::::::::::
151  TATAACTATGTCTCTCGTACCAACACCACCCAGGCAAGCCCCCAACT 200
   ::::::::::::::::::::::::::::::::::::::::::::::
51  ...AsnTrpValGlnTrpTyrGlnGlnArgValSerAlaProThrIle 66
   ::::::::::::::::::::::::::::::::::::::::::::::
201  CATGATTATGATCTCGCTAAGCGGGGCTCAGGGGTCTCTGATCGCTTCT 250
   :::::::::::::::::: ::::::::::::::::::::::::::::::
66  eValIleTyrGluAspAsnGlnArgProLeuGlyValProAspArgPheS 83
   :::::::::::::::::: ::::::::::::::::::::::::::::::
251  CTGGCTCG.....AAGTCGGCAACAGCGCTCCCTGACCATCTCTGGG 294
   :::::::::::::::::: ::::::::::::::::::::::::::::::
83  erGlySerIleAspSerSerAsnSerAlaSerLeuThrIleSerGly 99
   :::::::::::::::::: ::::::::::::::::::::::::::::::
295  CTCACGGCTCAGGACGAGGTGATTATTACTGTGTTCATATACAACACG 344
   :::::::::::::::::: ::::::::::::::::::::::::::::::
100  LeuLysThrGluaspGluAlaAspTyrTyrCysGlnSerPheaspAsnTh 116
   :::::::::::::::::: ::::::::::::::::::::::::::::::
345  TAGCATTCTGTTATTCGGAAGAGGACCCGGTTGACCGTCTCTAGGT 390
   :::::::::::::::::: ::::::::::::::::::::::::::::::
116  rAsnGlnGlyValPheGlyGlyThrLysLeuThrValLeuGly 131
   :::::::::::::::::: ::::::::::::::::::::::::::::::

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Sequence	Strd	Orig	zScore	EScore	Len	Documentation	...	
sp_human:Q96B61	+	427.50	785.50	8.9e-36	236	!	Q96e61	homo sapiens (human). ur
sp_human:Q96D1	+	329.50	609.91	1.1e-25	112	!	Q96d1	homo sapiens (human). ur
sp_human:Q96D30	+	328.00	606.82	1.6e-25	116	!	Q96d30	homo sapiens (human). an
sp_human:Q96B80	+	333.00	598.15	5.3e-25	108	!	Q96b80	homo sapiens (human). an
sp_human:Q96D2	+	317.00	586.69	2.2e-24	112	!	Q96d2	homo sapiens (human). an
sp_human:Q9NSD6	+	300.00	555.50	1.3e-22	107	!	Q9nsd6	homo sapiens (human). hy
sp_rodent:Q99W11	+	299.00	546.78	1.8e-22	235	!	Q99w11	mus musculus (mouse). hy
sp_human:Q96169	+	292.00	533.85	9.3e-22	233	!	Q96169	homo sapiens (human). ur
sp_human:Q9U182	+	286.50	530.42	3.2e-21	107	!	Q9U182	homo sapiens (human). my
sp_rodent:Q91V32	+	254.00	463.24	8.0e-18	233	!	Q91v32	m adult male small intestine (mouse). ur
sp_invertebrate:Q9U410	+	246.00	455.25	4.9e-17	106	!	Q9u410	schistosome japonicum (japanese katoxanthrozoan). ur
sp_human:Q9U181	+	241.50	446.81	1.4e-16	107	!	Q9U181	homo sapiens (human). my
sp_human:Q9U178	+	241.00	445.72	1.6e-16	109	!	Q9U178	homo sapiens (human). an
sp_human:Q96SA9	+	235.50	435.66	6.0e-16	107	!	Q96sa9	homo sapiens (human). an
sp_human:Q9U170	+	234.00	432.79	8.6e-16	108	!	Q9U170	homo sapiens (human). my
sp_human:Q9U177	+	233.00	430.93	1.1e-15	108	!	Q9U177	homo sapiens (human). my
sp_rodent:Q9JL78	+	231.00	427.80	1.7e-15	101	!	Q9Jl78	mus musculus (mouse). an
sp_rodent:Q9JL12	+	231.00	420.43	1.9e-15	235	!	Q9Jl12	mus musculus (mouse). ur
sp_rodent:Q9JL76	+	229.00	424.44	2.8e-15	97	!	Q9Jl76	mus musculus (mouse). an
sp_human:Q9U179	+	227.50	420.71	4.0e-15	108	!	Q9U179	homo sapiens (human). my
sp_rodent:Q9ER29	+	227.00	419.87	4.5e-15	107	!	Q9er29	mus musculus (mouse). an
sp_human:Q9U185	+	226.50	418.78	5.1e-15	109	!	Q9U185	homo sapiens (human). my
sp_human:Q9U186	+	224.00	414.13	9.3e-15	109	!	Q9U186	homo sapiens (human). my
sp_rodent:Q9QYF0	+	220.50	398.85	2.4e-14	298	!	Q9qyf0	mus musculus (mouse). cr
sp_mammal:Q9NW05	+	218.00	402.98	3.9e-14	109	!	Q9nw05	oryzctoleagus cuniculus (rabbit). ur
sp_rodent:Q9Z0E6	+	218.00	402.98	3.9e-14	109	!	Q9z0e6	mus musculus (mouse). pt
sp_rodent:Q91XK2	+	217.00	398.11	5.1e-14	154	!	Q91xk2	mus musculus (mouse). ad
sp_human:Q9U183	+	214.00	395.63	1.0e-13	108	!	Q9U183	homo sapiens (human). my
sp_rodent:Q9R1A5	+	214.00	389.66	1.1e-13	214	!	Q9r1a5	mus musculus (mouse). ka
sp_rodent:Q9Z0E9	+	212.00	391.68	1.6e-13	111	!	Q9z0e9	mus musculus (mouse). pt
sp_rodent:Q9ET13	+	211.00	389.98	2.1e-13	109	!	Q9et13	mus musculus (mouse). in
sp_rodent:Q9JWS9	+	209.50	380.56	3.2e-13	233	!	Q9jws9	mus musculus (mouse). hy
sp_rodent:Q99M37	+	208.00	377.59	4.6e-13	238	!	Q99m37	mus musculus (mouse). hy
sp_rodent:Q9JL82	+	207.50	383.88	4.7e-13	104	!	Q9Jl82	mus musculus (mouse). an
sp_rodent:Q91WF8	+	206.50	374.95	6.6e-13	234	!	Q91wf8	mus musculus (mouse). hy
sp_human:Q9U180	+	204.50	377.51	9.7e-13	114	!	Q9U180	homo sapiens (human). my
sp_human:Q9U176	+	200.50	371.85	2.5e-12	93	!	Q9U176	homo sapiens (human). myc
sp_rodent:Q9Z5S9	+	200.50	369.13	2.6e-12	127	!	Q9z5s9	mus musculus (mouse). in
sp_human:Q96PF6	+	200.00	369.02	2.9e-12	116	!	Q96pf6	homo sapiens (human). ka
sp_rodent:Q91XL0	+	200.00	363.78	3.1e-12	211	!	Q91xl0	mus musculus (mouse). ka

ID Q96JD1 PRELIMINARY; PRT; 112 AA.  
AC Q96JD1;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region PIP."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267874; AAK58586.1; -.  
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SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

alignment\_scores:  
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US-09-019-441-1 x Q96JD1 ..

Align seg 1/1 to: Q96JD1 from: 1 to: 112

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||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
5 ThrGlnProHisSerValSerGluSerProGlyThrIleThrIle 21  
120 CTGCACTGGAAACAGGATGACCTTGGTGGTTAATACTATGTCCTCGT 169  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
21 rCysThrArgSerSerGlySerIleAlaSer...AsnTyrValGlnTript 37  
170 ACCAACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCGCT 219  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
37 yrGlnGlnArgProGlySerAlaProThrThrValIleTyrGluAspAsn 53  
220 AAGCGGCGCTCAGGGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 263  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSerSe 70  
264 TGGCAACAGCGCTCCCTGACCATCTCTCTCTCTCTCTCTCTCTCTCT 313  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuLysThrGluAspGluA 87  
314 CTGATTATTACTCTTCTCATATACAAACAGT...AGCATTCTGTTATTC 363  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
87 laAspTyrTyrCysGlnSerTyrAspSerAsnAsnTyrAlaLeuPheGly 103  
364 AGAGGACCGCGTGTGACCGCTCTAGGT 390  
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104 GlyGlyThrGlnLeuThrValLeuGly 112

seq\_name: sp\_human:Q96JD0

seq\_documentation\_block:  
ID Q96JD0 PRELIMINARY; PRT; 116 AA.  
AC Q96JD0;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION SAR (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;

RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region SAR."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267875; AAK58587.1; -.  
FT NON\_TER 1 1  
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alignment\_scores:  
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US-09-019-441-1 x Q96JD0 ..

Align seg 1/1 to: Q96JD0 from: 1 to: 116

70 ACTCAGCCTCCCTCTGTCTGGTCTCTGGACAGTCGTCACCATCTC 119  
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5 ThrGlnProHisSerValSerGluSerProGlyLysThrValThrIleSe 21  
120 CTGCACTGGAAACAGGATGACCTTGGTGGTTAATACTATGTCCTCGT 169  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
21 rCysThrGlySerSerGlySerIle...AlaThrAsnTyrValGlnTript 37  
170 ACCAACACACCCAGGCAAGCCCAAACTCATGATTTATGATGTCGCT 219  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
37 yrGlnLeuArgProGlySerAlaProThrThrValIleTyrGluAspAsn 53  
220 AAGCGGCGCTCAGGGCTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 263  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSerSe 70  
264 TGGCAACAGCGCTCCCTGACCATCTCTCTCTCTCTCTCTCTCTCTCT 313  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuLysThrGluAspGluA 87  
314 CTGATTATTACTCTTCTCATATACAAACAGT...AGCATTCTGTTATTC 360  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
87 laAspTyrTyrCysGlnSerTyrAspSerIleGlyAsnValIlePhe 103  
361 GGNAGAGGACCGGTTGACCGCTCTAGGT 390  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
104 GlyGlyThrLysLeuThrValLeuGly 113

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seq\_documentation\_block:  
ID Q96SB0 PRELIMINARY; PRT; 108 AA.

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DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN  
DE VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=98375893; PubMed=9712075;  
RX Adderson E.E., Shikhman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal monoclonal antibodies from  
rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
antibody V region genes".  
RT J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96394; AAB68783.1; -.



FT NON\_TER 1 1  
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

## alignment\_scores:

Quality: 323.00 Length: 109  
Ratio: 3.589 Gaps: 3  
Percent Similarity: 82.569 Percent Identity: 61.468

## alignment\_block:

US-09-019-441-1 x Q96SB0 ..

Align seg 1/1 to: Q96SB0 from: 1 to: 108

58 CAGTCTGCCGAGTACAGCTCCCTCTGTCTGTGGTCTCTGACAGTC 107  
1 GlnSerValLeuThrGlnProSerAlaSerGlyThrProGlyGlnAr 17  
108 GGTACCATCTCCTGCACCTGGAACGAGGATGAGCTTGCTGTATAC 157  
17 gValThrIleSerCysSerGlySerSerAsnIleGlySer...AsnT 33  
158 ATGTCTCTCTGTACCAACACCCAGGCAAGCCCAACTCATGATT 207  
33 yrValTyTriPtyrGlnGlnLeuProGlyThrAlaProLysLeuLeu 49  
208 TATGATGTCTGTAAGCGGCTCAGGGTCTCTGATCCTCTCTGGCTC 257  
50 TyrArgAsnAsnGlnArgProSerGlyValProAspArgPheSerGly 66  
258 CAAGTCTGCAACAGCGGCTCCCTGACCATCTCTGGCTCAGGCTGAG 307  
66 rLysSerGlyThrSerAlaSerLeuAlaIleSerGlyLeuArgSerGluA 83  
308 ACGAGCTGATTATTACTGTCTTCATAT.....ACAACCATGAGC 348  
83 spGluAlaAspTyTyrCysAlaAlaTrpAspArgLeuSerGly.Ph 99  
349 ACTTTGTATTCTGGAGAGGACCC 373  
99 eMetTrpTySerAlaGlyPro 107

seq\_name: sp\_human:Q96JD2

## seq\_documentation\_block:

ID Q96JD2 PRELIMINARY; PRT; 112 AA.  
AC Q96JD2;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE ANYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BONE MARROW;  
RA Perletti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Anyloid lambda 6 light chain variable region NEG."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF267873; AAK58585.1;  
FT NON\_TER 1 1  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

## alignment\_scores:

Quality: 317.00 Length: 109  
Ratio: 3.446 Gaps: 3  
Percent Similarity: 84.404 Percent Identity: 60.550

## alignment\_block:

70 ACTCAGCCTCCCTCTGTCTGTGGTCTCTGACAGTCGGTCACCATCTC 119

US-09-019-441-1 x Q96JD2 ..

Align seg 1/1 to: Q96JD2 from: 1 to: 112

70 ACTCAGCCTCCCTCTGTCTGTGGTCTCTGACAGTCGGTCACCATCTC 119  
5 ThrGlnProHisSerValSerGlySerProGlyLysThrIleThrIleSe 21  
120 CTGCACCTGGAAACACGAGGATGACGTGGTGGTTATTAACATATCTC 169  
21 rCysThrGlySerGlyArgIleAlaSer...AsnSerValGlnTrpT 37  
170 ACCAACACCCAGGCAAGCCCAACTCATGATTATGATGTCGCT 219  
37 yrGlnGlnArgProGlySerAlaProAsnIleValMetTyfGluAsn 53  
220 AAGCGGCTCAGGGTCTCTGATCGTCTCTGGCTCC.....AAGTC 263  
54 GlnArgProSerGlyValProAspArgPheSerGlySerIleAspSer 70  
264 TGGCAACAGCGCTCCCTGACCATCTCTGGGCTCCAGGCTCAGGAGG 313  
70 rSerAsnSerAlaSerLeuThrIleSerGlyLeuMetThrGluAspGlu 87  
314 CTGATTATTACTGTGTTCATATACACCATGACACTTTG...TTATTC 360  
87 laAspTyTyrCysGlnSerPheAspSerThrAsnGlnGlyValPhe 103  
361 GGAAGAGGAGCGGCTTGACCGTCTCTA 387  
104 GlyGlyThrArgLeuThrValLeu 112

seq\_name: sp\_human:Q9NSD6

## seq\_documentation\_block:

ID Q9NSD6 PRELIMINARY; PRT; 107 AA.  
AC Q9NSD6;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LYMPHOCYTE;  
RA Hohmann A.;  
RT "Autoimmunity".  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
DR EMBL: L43092; AAA69746.2; -.  
DR HSSP: P01709; 2MCG.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; ig; 1.  
DR SMART: SM00406; IGV; 1.  
FT NON\_TER 1 1  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11306 MW; A2B04B37187A5F00 CRC64;

## alignment\_scores:

Quality: 300.00 Length: 108  
Ratio: 3.571 Gaps: 3  
Percent Similarity: 77.778 Percent Identity: 60.185

## alignment\_block:

US-09-019-441-1 x Q9NSD6 ..

Align seg 1/1 to: Q9NSD6 from: 1 to: 107

```

||||| ||| ||||| :||| |||||:||||| |||||
3 ThrGlnaspProValValSerValAlaLeuGlyGlnThrValArgIleTh 19
120 CTGCACCTGGAAACAGCAGGATGCTGGTTATAAATATGCTCTCCGGT 169
:||||| ||| |||||:||||| |||||:||||| |||||
19 rCysGlnGly.....AspSerLeuArgSerTyr...TyrAlaSerIrpT 33
170 ACCAACACACCCAGGCAAGCCCAACATCATGATTATGATGTCGCT 219
33 yrGlnGlnLysProGlyGlnAlaProValLeuValIleTyrGlyLysAsn 49
220 AAGCGGCGCTCAGGGGCTCTGATCGCTTCTCGGCTCCAGTCTGGCAA 269
:||||| |||||:||||| |||||:||||| |||||
50 AsnArgProSerGlyIleProAspArgPheSerGlySerSerGlyAs 66
270 CACGGCTCCTCGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATT 319
||||| ||| |||||:||||| |||||:||||| |||||
66 nThrAlaSerLeuThrIleThrGlyAlaGlnAlaGluAspGluAlaAspT 83
320 ATTACTGTGTCATATACACACAGTACGACT...TTGTTATTCGGAAGA 366
||||| ||| |||||:||||| |||||:||||| |||||
83 yrTyrCysAsnSerArgAspSerSerglyAsnHisAlaValPheGlyGly 99
367 GGGACCGGTTGACCGCTCCTAGGT 390
|||||:||||| ||||| |||||
100 GlyThrLysLeuThrValLeuGly 107

```

seq\_name: sp\_rodent:Q99M11

```

seq_documentation_block:
ID Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 25.4 KDA PROTEIN.
OS Mus musculus (mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002129; AAH02129.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 1.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

```

```

alignment_scores:
  Quality: 299.00      Length: 131
  Ratio: 2.990        Gaps: 3
Percent Similarity: 76.336      Percent Identity: 51.145

alignment_block:
US-09-019-441-1 x Q99M11 ..
Align seg 1/1 to: Q99M11 from: 1 to: 235

1 ATGGCCTGGACTCTGCTCCGTCACCCCTCTCTACTCAGGCGACAGGATC 50
|||||:||||| |||||:|||||:||||| |||||

```

```

1 MetThrTrpAlaProLeuLeuLeuValPheLeuHisLeuThrGlySe 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCCTCTGTCTGTGGTCTCTCG 100
||||| :||| ||||| ||||| ||||| |||||
17 rCysAlaGlnLeuValLeuThrGlnProSerSerValSerThrSerLeuG 34
101 GACAGTCGGTCACCATCTCTCGCACTGGAACACGCGATGACGTTGGT 150
|||||:||||| ||| |||||:||||| |||||
34 lySerThrAlaLysLeuProCysLysAlaSerThrGlyAsnIleGlyAsp 50
151 TATAACTATGTCCTCGGTACCAACACACCCAGGCAAGCCCAAACT 200
:|||||:||||| |||||:||||| |||||
51 ...SerTyrValAsnTrpTyrGlnGlnTyrMetGlyArgSerProThrAs 66
201 CATGATTATGATGTCGCTAAGCGGCTCAGGGGCTCTGAGTCGCTTCT 250
||||| ||| ||||| ||||| ||||| |||||
66 nMetIleTyrGlyAspAspLeuArgProSerGlyValSerAspArgPheS 83
251 CTGGCTCC.....AGTCTGGCAACACGCGCTCCCTGACCATCTCTGG 294
||||| ||| |||||:||||| |||||:||||| |||||
83 erGlySerIleAspSerSerSerAsnSerAlaPheLeuThrIleGlnAsn 99
295 CTCGAGCTGAGGACGAGGCTGATTATTACTGTGTTCATATACAAACAG 344
:|||||:||||| ||||| ||||| ||||| |||||
100 ValGlnAlaAspAspGluAlaAspTyrTyrCysGlnSerTyr...SerSe 115
345 TAGCAGCTTTGTTATTCGGAAGAGGACCGGTTGACCGCTCTA 387
|||: ||| ||||| |||||:||||| ||||| |||||
115 rGlyIleArgValPheGlyGlyGlyThrLysLeuThrValLeu 129

```

seq\_name: sp\_human:Q96I69

```

seq_documentation_block:
ID Q96I69 PRELIMINARY; PRT; 233 AA.
AC Q96I69;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:12849).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007782; AAH07782.1; -.
SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

```

```

alignment_scores:
  Quality: 292.00      Length: 131
  Ratio: 2.949        Gaps: 2
Percent Similarity: 75.573      Percent Identity: 48.092

alignment_block:
US-09-019-441-1 x Q96I69 ..
Align seg 1/1 to: Q96I69 from: 1 to: 233

1 ATGGCCTGGACTCTGCTCCGTCACCCCTCTCTACTCAGGCGACAGGATC 50
|||||:||||| |||||:|||||:||||| |||||
1 MetAlaTrpThrValLeuLeuLeuGlyLeuLeuSerHisCysThrGlySe 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCCTCTCTGTCTGTGGTCTCTCG 100
|||||:||||| ||| |||||:||||| |||||
17 rGlyThrSerTyrValLeuThrGlnProAlaSerValSerValAlaProG 34
101 GACAGTCGGTCACCATCTCTGCACTGGAACACGCGATGACGTTGGTGGT 150
|||||:||||| ||||| ||||| ||||| |||||
34 lyGlnThrAlaArgIleThrCysGlyGlySerAsn.....LeuGly 47

```

```

alignment_scores:
  Quality: 286.50      Length: 106
  Ratio: 3.411         Gaps: 1
  Percent Similarity: 79.245      Percent Identity: 53.774

alignment_block:
  US-09-019-441-1 x Q9UL82      ..

  Align seg 1/1 to: Q9UL82 from: 1 to: 107

70  ACTCAGCGTCCCTCTGTGTCTGGGTCTCTCTGGACAGTCGGTCACCATCTC 119
   |||||
5  ThrGlnProSerValSerProGlyGlnThrAlaAargileh 21
   |||||

120 CTCGACTGGAAACCGATGACGCTTGGTGGTTATACTATGTCCTCGT 169
   |||||
21 rCYSerGly.....AspLeuLeuAlaLysLysTyraAlaArgTrpP 35
   |||||

170 ACCAACACCAACCCAGCAAGCCGCCCAAACTCATGATTTTATGATGTCGCT 219

```



OX		NCBI_TaxID=9606;	
RN	[1]		
RP		SEQUENCE FROM N.A.	
RX		MEDLINE=98277139; Pubmed=9614934;	
RA		Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,	
RT		Young D.C.;	
RR		"Myosin-reactive autoantibodies in rheumatic carditis and normal	
RT		fetus.";	
RL		Clin. Immunol. Immunopathol. 87:184-192(1998).	
RD		EMBL: AF035033; RAD56269.1; -	
DR	HSSP:	P01607. 1REI	
DR		InterPro: IPR003006; Ig_MHC.	
DR		InterPro: IPR003596; Ig_v.	
DR		Pfam: PF00047; Ig_1.	
DR		SMART: SM00406; Igv; 1.	
FT		NON_TER 1	
FT		NON_TER 107	
FT		SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;	
SQ			

alignment_scores:		
Quality:	241.50	Length: 103
Ratio:	3.096	Gaps: 3
Percent Similarity:	75.728	Percent Identity: 51.456

alignment block:

US-09-019-441-1 x 09UL81

Align seq 1/1 to: Q9UL81 from: 1 to: 107

[illegible]

seq\_name: sp\_human:Q9UL78

seq_documentation_block:	PRELIMINARY;	PRT;	109 AA.
ID Q9UL78			
AC Q9UL78;			
DC DT	01-MAY-2000 (TrEMBLrel. 13, Created)		
DT DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)		
DT DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION		

OS Homo sapiens (Human) .  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]

RP	SEQUENCE FROM N.A.
RX	MEDLINE=98277139; PubMed=9614934;
RA	Wu X., Liu B., Van der Merve P.L., Kalis N.N., Berney S.M.,
RA	Young D.C.;
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal
RT	fetus.";
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).
DR	ENBL; AF035036; AAD56272.1; -
DR	HSP; P80362; 1WTL.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_v.
DR	Pfam: PF00047; ig; 1.
DR	SMART: SM00406; Igv; 1.
FT	NON_TER 1
FT	NON_TER 109
SO	SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

alignment_scores:		
Quality:	241.00	Length: 106
Ratio:	2.939	Gaps: 4
Percent Similarity:	77.358	Percent Identity: 50.000

alignment block:

US-09-019-441-1 x Q9UL78

Align seq 1/1 to: 09UL78 from: 1 to: 109

```

70  ACTCAGCCTCCC...TCGTGTCTCTGGGTCTCTCGAGACAGTCGGTCCACCAT 116
      ||||| ||| ::::||||| ||||| ||||| ::::||||| :||| :||| :|||
5  ThrGlnSerProGlyThrLeuSerLeuSerProGlyGluArgAlaThrLeu 21
      ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117 CNCCTGCACCTGGACACCGATGACGTCGTGGTGTATTAAGTATGTCCTCT 166
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
21  userCysArg...AlaSerGlnSerValSerSer...SerTyrLeuAlaIar 36
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
167 GGTACCAACACACACCGACGCAAGCCGCCAAACTCATGATTATTATGATGTC 216
      ||||| ||||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
36  rPtyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrGlyAla 52
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
217 GCTAAGCGGGCCTCAGGGGTCTCTGATCGCTCTCTCTGGCTCCAAGTCCTGG 266
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
53  SerSerArgAlaThrGlyIleProAspArgPheSerGlySerGlySerGly 69
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
267 CAACAGCGCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGCGTG 316
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
69  YThrAspPheThrLeuThrIleSerArgLeuGluProGluAspCysAlaVal 86
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
317 ATTATTACTGTGTTTCATATACACCACTAGCAGCTTGTATTTCGGAAGA 366
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
86  alTyrTyrCysGlnGlnTyr...GlySerSerProLeuThrPheGlyGly 101
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
367 GGGACCGCGTTGACCGTC 384
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
102 GivThrLysValGluIle 107
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

seq\_name: sp human:O96SA9

seq documentation block:

```
seq_documentation_block.
ID 096SA9 PRELIMINARY: PRT: 107 AA.
```

Q958A9;  
01-DEC-2001 (TrEMBLrel. 19, Created)  
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN  
VARIABLE REGION (FRAGMENT).  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi  
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=98375893; PubMed=9712075;

RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody v region genes";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96396; AAB68785.1; -;  
FT NON\_TER 1 1  
FT NON\_TER 107 107  
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E5C5B577F16 CRC64;

alignment\_scores:  
Quality: 235.50 Length: 103  
Ratio: 3.058 Gaps: 3  
Percent Similarity: 74.757 Percent Identity: 50.485

alignment\_block:

US-09-019-441-1 x Q96SA9 ..

Align seg 1/1 to: Q96SA9 from: 1 to: 107

```
76 CCTCCCTCTGTCTGGTCTCTGGACAGTCGTCACCATCTCCTGCAC 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   8 ProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysAr 24
126 TGAACACGAGATGACGTTGGTGGTTATAACTATGTCCTCGTGTACCAAC 175
   ::::::::::::::::::::
   24 g...AlaSerGlnSerIleSer.....SerTyrLeuAsnTyrTyrGlnG 38
176 ACCACCCAGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGG 225
   :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   38 InLysProGlyLysAlaProLysLeuLeuIleTyrAlaAlaSerSerLeu 54
226 GCCTCAGGGTCTCTGATGCTCTCTGGCTCCCAAGTCTGGCAACACGGC 275
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   55 GlnSerGlyValProSerArgPheSerGlySerGlySerGlyThrAspPh 71
276 CTCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACT 325
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   71 eThrLeuThrIleSerSerLeuGlnProGluAspPheAlaThrTyrTyrC 88
326 GTTGTTTCATATACACAGTAGCATTGTTATTTCGAGAGGAGGACCCGG 375
   || ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
   88 ys.....GlnGlnSerTyrSerThrLeuThrPheGlyGlyThrLys 102
376 TTGACCGTC 384
   ||| |||
103 ValGluIle 105
```

seq\_name: sp\_human:Q9UL70

seq\_documentation\_block:  
ID Q9UL70 PRELIMINARY; PRT; 108 AA.  
AC Q9UL70;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035044; AAD56280.1; -;  
DR HSSP; P01607; IREI.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.  
FT NON\_TER 1 108  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

alignment\_scores:  
Quality: 234.00 Length: 103  
Ratio: 3.162 Gaps: 2  
Percent Similarity: 71.845 Percent Identity: 49.515

alignment\_block:  
US-09-019-441-1 x Q9UL70 ..

Align seg 1/1 to: Q9UL70 from: 1 to: 108

```
76 CCTCCCTCTGTCTGGTCTCTGGACAGTCGTCACCATCTCCTGCAC 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   8 ProSerSerLeuSerAlaSerValGlyAspArgValThrIleThrCysAr 24
126 TGAACACGAGATGACGTTGGTGGTTATAACTATGTCCTCGTGTACCAAC 175
   ::::::::::::::::::::
   24 gAlaSerGln.....GlyIleSerAsnTyrLeuAlaThrTyrGlnG 38
176 ACCACCCAGCAAGCCCCCAACTCATGATTTATGATGTCGCTAAGCGG 225
   :: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   38 InLysProGlyLysValProLysSerLeuIleTyrAlaAlaSerThrLeu 54
226 GCCTCAGGGTCTCTGATGCTCTCTGGCTCCCAAGTCTGGCAACACGGC 275
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   55 GlnSerGlyValProSerArgPheSerGlySerGlySerGlyThrAspPh 71
276 CTCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACT 325
   ::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
   71 eThrLeuThrIleSerSerLeuGlnProGluAspValAlaThrTyrTyrC 88
326 GTTGTTTCATATACACAGTAGCATTGTTATTTCGAGAGGAGGACCCGG 375
   || ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
   88 ysGlnLysTyr...AsnSerAlaProArgThrPheGlyProGlyThrLys 103
376 TTGACCGTC 384
   ||| |||
104 LeuGluIle 106
```

seq\_name: /can2\_6/ptodata/2/paa/PCTUS\_COMB.pep:PCT-US01-08631-49652





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seq_name: /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:PCT-US01-08631-43245
seq_documentation_block:
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; Sequence 43245, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; FILE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 43245
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (168)..(191)
; OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00290A, p-value=
; OTHER INFORMATION: 1.529e-14, raw score of 20.89
; PCT-US01-08631-43245

alignment_scores:
  Quality: 557.00      Length: 130
  Ratio: 4.528        Gaps: 0
  Percent Similarity: 94.615      Percent Identity: 80.000

alignment_block:
US-09-019-441-1 x PCT-US01-08631-43245      ..
Align seg 1/1 to: PCT-US01-08631-43245      from: 1 to: 249

1  ATGGCTGGACTGTCTCTCGTCACCCCTCCTCACTCAGGGCACAGATC 50
15 MetAlaTrpAlaLeuLeuIleLeuThrLeuLeuThrGlnGlyThrGly 31
51 CTGGGCTCAGTCGCCCGCAGCTCCCTCTGTCTGTGGTCTCTCTG 100
31 rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeu 48
101 GACAGTCGGTCACCACTCTCTGACCTGGACGACGATGACGTGTGGT 150
48 lGlnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 64
151 TATAACTATGTCCTCTGGTACCAACACCCAGGCAAGCCCAAACT 200
65 TyrAsnTyrValSerTyrPyrArgGlnHisProGlyLysAlaProLysLe 81
201 CATGATTATGATGCTGAAGCGGCTCAGGGTCTCTGATCGCTTCT 250
81 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPhe 98
251 CTGGCTCCAGTCTGCAACACCGCTCCCTGACCATCTCTGGGCTCCAG 300
98 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 114
301 GCTGAGACGAGGCTGATTATTACTTGTTCATACCAACACCATAGCAC 350
115 AlaGluAspLysAlaSerTyrCysSerSerTyrAlaGlySerAsnSe 131
351 TTGTGTTATTCGGAAGAGGACCGGTGACCGTCCCTAGGT 390
131 rLeuIlePheGlyGlyThrArgLeuThrValLeuGly 144

seq_name: /cgn2_6/ptodata/2/paa/US090_COMB.pap:US-09-049-672-10
seq_documentation_block:
; Sequence 10, Application US/09049672
; GENERAL INFORMATION:
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51  TyrAsnTyrValSerTrpTyrGlnGlnSerProGlyThrAlaProLysLe 67
201 CATGATTATATGCTCGCTAAGCGGGCTCAGGGTCTCTGATCGCTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  uMetIleTyrGluValSerAsnArgProSerGlyValSerAsnArgPheS 84
251 CTGGCTCCAGCTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301 GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAAACCATAGCAC 350
101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValGlyAsnAsnI 117
351 TTTGTTATTCGGAAGAGGACCGGCTGACCGTCTCTAGGT 390
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 eValValPheGlyGlyGlyThrLysLeuThrValLeuGly 130
seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-186-656-1041
seq_documentation_block:
; Sequence 1041, Application US/60186656
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000320
; CURRENT APPLICATION NUMBER: US/60/186,656
; CURRENT FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 1518
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1041
; LENGTH: 118
; TYPE: PRT
; ORGANISM: HUMAN
US-60-186-656-1041

alignment_scores:
  Quality: 549.00      Length: 118
  Ratio: 4.816        Gaps: 0
  Percent Similarity: 96.610      Percent Identity: 88.136

alignment_block:
US-09-019-441-1 x US-60-186-656-1041  ..
Align seg 1/1 to: US-60-186-656-1041 from: 1 to: 118
1  ATGGCTGGACTCTGCTCTCGTCACCTCCTCACTCAGGCACAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1  MetAlaTrpAlaLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlyse 17
51  CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGGCTCTCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34
101  GACAGTCGGTCACCATCTCTGCTGACTGGAACACGACGATGAGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly 50
151  TATRACTATGCTCTCTGGTACCAACACACCCAGGCAAGCCCCCAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67
201  CATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCTGATCGCTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS 84
251  CTGGCTCCAGCTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301  GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAAACCATAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValSerSerSerTh 117
351  TTTG 354
|||||
```

```
301  GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAAACCATAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValSerSerSerTh 117
351  TTTG 354
|||||
117  rLeu 118
seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-187-385-551
seq_documentation_block:
; Sequence 551, Application US/60187385
; GENERAL INFORMATION:
; APPLICANT: Bonazzi, Vivien
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000334
; CURRENT APPLICATION NUMBER: US/60/187,385
; CURRENT FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 922
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 551
; LENGTH: 121
; TYPE: PRT
; ORGANISM: HUMAN
; NAME/KEY: VARIANT
; LOCATION: (1)...(121)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-187-385-551

alignment_scores:
  Quality: 549.00      Length: 118
  Ratio: 4.816        Gaps: 0
  Percent Similarity: 96.610      Percent Identity: 88.136

alignment_block:
US-09-019-441-1 x US-60-187-385-551  ..
Align seg 1/1 to: US-60-187-385-551 from: 1 to: 121
1  ATGGCTGGACTCTGCTCTCGTCACCTCCTCACTCAGGCACAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1  MetAlaTrpAlaLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlyse 17
51  CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGTCTGGGCTCTCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34
101  GACAGTCGGTCACCATCTCTGCTGACTGGAACACGACGATGAGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyGly 50
151  TATRACTATGCTCTCTGGTACCAACACACCCAGGCAAGCCCCCAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67
201  CATGATTATGATGTCGCTAAGCGGGCTCAGGGGTCTCTGATCGCTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS 84
251  CTGGCTCCAGCTCTGGCAACACGGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301  GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAAACCATAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrValSerSerSerTh 117
351  TTTG 354
|||||
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117 rLeu 118

seq\_name: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep: PCT-US01-08631-43243

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seq_documentation_block:
; Sequence 43243, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 43243
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (86)..(120)
; OTHER INFORMATION: IMMUNOGLOBULIN V REGION domain identified by eMATRIX,
; OTHER INFORMATION: accession number DM00031B, p-value=5.329e-09, raw score of 15.41
PCT-US01-08631-43243
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alignment_scores:
  Quality: 548.00      Length: 130
  Ratio: 4.567         Gaps: 0
Percent Similarity: 92.308      Percent Identity: 78.462
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alignment\_block:  
US-09-019-441-1 x PCT-US01-08631-43243

Align seg 1/1 to: PCT-US01-08631-43243 from: 1 to: 151

```
1  ATGGCTGGACTGCTCTCGTCACCCCTCTCACTCAGGGCACAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
9  MetAlaTrpAlaLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlyse 25
51  CTGGGCTCAGTCTGCCCGCAGCTCAGCTCCCTCTGTCTGTGGTCTCCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25  rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 42
101 GACAGTCGGTCACCACTCTCTGACCTGGACCGATGACGTTGCTGTT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
42  lYglnSerIleThrIleSerCysThrGlyThrSerAsnAspValGlyGly 58
151 TATACTATGTCCTCGTACCAACACCCAGGCAAGCCCAAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
59  TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProGluLe 75
201 CATGATTATGATGTCGTAAGCGGCCTCAGGGTCTCTGATCGGTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
75  uIleIlePheAspValSerAsnArgProLeuGlyValSerThrArgPheS 92
251 CTGGCTCCCAAGTCTGGCAACACAGCCCTCCCTGACCATCTCTGGGCTCC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92  erGlySerLysSerGlyIleMetAlaSerLeuThrIleSerGlyLeuGln 108
301 GCTGAGGACGAGCTGATTATTACTTGTTCATATACAACTAGTAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
109  AlaGluAspGluAlaAspTyrTyrCysSerPheThrSerArgAsnSe 125
351 TTGTTATTGGGAAGAGACCGCGTTGACCGCTCCTAGGT 390
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
125  rArgValPheGlySerGlyThrLysValThrValLeuGly 138
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seq\_name: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep: PCT-US01-08631-49650

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seq_documentation_block:
; Sequence 49650, Application PC/TUS0108631
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 21272-049
; CURRENT APPLICATION NUMBER: PCT/US01/08631
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 49650
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (170)..(193)
; OTHER INFORMATION: Immunoglobulins and major histocompatibility complex proteins
; OTHER INFORMATION: domain identified by eMATRIX, accession number BL00290A, p-val
; OTHER INFORMATION: 1.529e-14, raw score of 20.89
; NAME/KEY: DOMAIN
; LOCATION: (48)..(234)
; OTHER INFORMATION: Immunoglobulin domain identified by Pfam, accession name Ig,
; OTHER INFORMATION: E-value=3e-18, Pfam score of 63.8
PCT-US01-08631-49650
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alignment_scores:
  Quality: 546.00      Length: 132
  Ratio: 4.439         Gaps: 1
Percent Similarity: 93.182      Percent Identity: 78.030
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alignment\_block:  
US-09-019-441-1 x PCT-US01-08631-49650

Align seg 1/1 to: PCT-US01-08631-49650 from: 1 to: 251

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1  ATGGCTGGACTGCTCTCGTCACCCCTCTCACTCAGGGCACAGGATC 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
15  MetAlaTrpAlaLeuLeuIleLeuThrLeuLeuThrGlnGlyThrGlyse 31
51  CTGGGCTCAGTCTGCCCGCAGCTCAGCTCCCTCTGTCTGTGGTCTCCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31  rTrpAlaGlnSerAlaLeuThrGlnProProSerAlaSerGlySerLeuG 48
101 GACAGTCGGTCACCACTCTCTGACCTGGAAACCGATGACGTTGTTGTT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
48  lYglnSerValThrPheSerCysSerGlyThrSerSerAspIleGlyAsn 64
151 TATACTATGTCCTCGTACCAACACCCAGGCAAGCCCAAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65  TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysLe 81
201 CATGATTATGATGTCGTAAGCGGCCTCAGGGTCTCTGATCGGTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
81  uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS 98
251 CTGGCTCCCAAGTCTGGCAACACAGCCCTCCCTGACCATCTCTGGGCTCC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
98  erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 114
301 GCTGAGGACGAGCTGATTATTACTTGTTCATATACAACTAGTAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115  AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlyAspTyrThr 131
351 T.....TTGTTATTGGGAAGAGACCGCGTTGACCGCTCCTAGGT 390
: |||||:|||||:|||||:|||||:|||||:|||||:|||||:
131  rProGlyValValPheGlyGlyGlyThrLysLeuThrValLeuGly 146
```







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; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 85829
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-85829

alignment_scores:
    Quality: 570.00      Length: 129
    Ratio: 4.711        Gaps: 0
    Percent Similarity: 93.798    Percent Identity: 84.496

alignment_block:
US-09-019-441-1 x US-09-791-537-85829  ..

Align seg 1/1 to: US-09-791-537-85829 from: 1 to: 130

1  ATGGCCCTGGAGCTGTCTCTGTCACCCCTCCTCACTCAGGGCACAGGATC 50
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  MetaLarPserProLeuPheLeuPheLeuThrGlnGlyThrGlySe 17

51  CTGGGCTCAGTCTGCCCGGACCTACGCTCCCTCTGTGTGGTCTCTCG 100
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  rTPAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

101  GACAGTCCGGTCACCATCTCTCTGCACATGGACACGAGGATGACGTTGGTGGT 150
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlyCly 50

151  TATAACTATATCTCTCGGTACCAACACCACCGAGCAAGGCCCAAACT 200
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  TyrAsnTyrValSerTrpTyrGlnHisProGlyLysAlaProLysLe 67

201  CATGATTTATGATGTCTGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTCT 250
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  uMetIleTyrAspValSerAsnArgProSerGlyValSerAsnArgPheS 84

251  CTGGCTCCAAAGTCTGGCAACAGGGCTCCCTGACCATCTCTGGGCTCCAG 300
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  erGlySerLysSerAspAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301  GCTGAGGACGAGGCTGATTATCTACTGTTGTTTCATATACACCACTAGCAC 350
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  AlaGluAspGluAlaAspTyrTyrCysSerSerTyrThrSerSerSerTh 117

351  TTTCGTTATTCCGAAGAGGGACCGCGGTGACCGTCCCTA 387
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117  rLeuValPheGlyGlyGlyThrLysLeuThrValLeu 129

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139061

seq_documentation_block:
; Sequence 139061_Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791.537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139061
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-139061

```





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101 GACAGTCGGTCACCATCTCTGCACTGGAACACCGCATGACGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 LyGlnSerValThrPheSerCysSerGlyThrSerAspIleGlyAsn 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 TATACTATGTCCTCGGTACCAACACCGACCGGAAAGCCGCCAAACT 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 TyrAsnTyrValSerTrpTyrArgGlnHisProGlyLysAlaProLysLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 CATGATTATGATGTCCTCAAGGGGCGCTCAGGGGTCTCTGATCGCTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 uMetIleTyrGluValThrLysArgProSerGlyValProAsnArgPheS 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 CTGCTCCAAAGTGGCAACACCGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrValSerGlyLeuGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 GCTGAGCAGCAGCTGATTATTACTGTGTTCATATACACACAGTAGCAC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 AlaGluAspGluAlaAspTyrTyrCysSerSerTyrAlaGlySerAsnSe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
351 TTTGTTATTTCGGAAGGAGCGGTTGACCGTCCTAGGT 390
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 rLeuIlePheGlyGlyThrArgLeuThrValLeuGly 130
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-120441
seq_documentation_block:
; Sequence 120441, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 120441
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-120441
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alignment_scores:
  Quality: 547.00      Length: 119
  Ratio: 4.798        Gaps: 0
  Percent Similarity: 95.798      Percent Identity: 86.555
alignment_block:
US-09-019-441-1 x US-09-791-537-120441
Align seg 1/1 to: US-09-791-537-120441 from: 1 to: 136
34 ACTCAGGCGCAGGATCCTGGGCTCAGTCTGCCCGGACTCAGCTCCCTC 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ThrGlnGlyThrGlySerTrpAlaGlnSerAlaLeuThrGlnProAlaSe 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 TGTGTCGGTCTCTCGGACAGTCGGTCACCATCTCTCGTCACTGGAACCA 133
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rValSerGlySerProGlyGlnSerIleThrIleSerCysThrGlyThrs 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 GCATGACGTTGGTGGTTAATACTATGTCCTCGGTACCAACACCAACCCA 183
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 erSerAspValGlyGlyTyrAsnTyrValSerTrpTyrGlnGlnHisPro 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
184 GGCAAGCCCCCAAACTCATGATTTATGATCGCTAAGCGGCGCTCAGG 233
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 GlyLysAlaProLysLeuMetIleTyrAspValSerAsnArgProSerGI 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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```
234 GGTCTCTGATCGCTTCTCTGGCTCCCAAGTCTGGCAACACCGCCTCCCTGA 283
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 yValSerAsnArgPheSerGlySerLysSerGlyAsnThrAlaSerLeuT 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
284 CCATCTCTGGGCTCCAGGCTGAGGAGGAGGCTGATTATTACTGTGTTC 333
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 hrIleSerGlyLeuGlnAlaGluAspGluAlaAspTyrTyrCysSerSer 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
334 TATACACACAGTAGCAGCTTTGTTATTTCGGAAGAGGAGCCGGTTGACCGT 383
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 TyrThrSerSerSerValValPheGlyGlyGlyThrLysLeuThrVa 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
384 CCTAGGT 390
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 lLeuGly 119
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-91653
seq_documentation_block:
; Sequence 91653, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 91653
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-91653
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alignment_scores:
  Quality: 546.00      Length: 130
  Ratio: 4.627        Gaps: 0
  Percent Similarity: 90.769      Percent Identity: 80.769
alignment_block:
US-09-019-441-1 x US-09-791-537-91653
Align seg 1/1 to: US-09-791-537-91653 from: 1 to: 235
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1 ATGGCTGTGACTCTGCTCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 50
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1 MetAlaTrpAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 CTGGGCTCAGTCTGCCCGGACTCAGCTCCCTCTGTGTCTGTGGTCTCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaPheValSerGlySerProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 GACAGTCGGTCACTCTCCTGCACTGGAACACCGCATGACGTTGGTGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 lYArgSerIleAlaIleSerCysThrGlyThrSerSerAspValGlySer 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 TATACTATGTCCTCGGTACCAACACCGGAGGAGGAGGAGGAGGAGGAGG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 TyrAsnLeuValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
201 CATGATTATGATGTCGCTAAGCGGCGCTCAGGGGTCTCTGATCGCTTCT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 uMetIleTyrGlnGlySerLysArgProSerGlyValSerIleArgPheS 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
251 CTGGCTCCCAAGTCTGGCAACACCGCTCCCTGACCATCTCTGGGCTCCAG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 GCTGAGCAGCAGCTGATTATTACTGTGTTCATATACACACAGTAGCAC 350
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; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 120444  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-120444

alignment\_scores:  
Quality: 540.00 Length: 119  
Ratio: 4.779 Gaps: 0  
Percent Similarity: 94.958 Percent Identity: 84.874

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Align seg 1/1 to: US-09-791-537-120444 from: 1 to: 137

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1 ThrGlnGlyThrGlySerTrpAlaGlnSerAlaLeuThrGlnProSe 17  
84 TGTCTCTGGTCTCCTGGACAGTCGGTCACATCTCTGCACGTGAACCA 133  
|||||  
17 rAlaSerGlySerProGlyGlnSerValThrIleSerCysThrGlyThrS 34  
134 GCGATGACGTTGGTGTATAACTCTCTGGTACCAACACCCCA 183  
|||||  
34 erSerAspValGlyGlyTyrAsnTyrValSerIleGlnHisPro 50  
184 GGCAAGCCCCCAACTCATGATTATGATCGTCAAGCGGCGCTCAGG 233  
|||||  
51 GlyLysAlaProLysLeuMetIleTyrGluValSerLysArgProSerG 67  
234 GGTCTCTGATCGTCTCTGGCTCCAAGTCTGGCAACACGCGCTCCCTGA 283  
|||||  
67 yValProAspArgPheSerGlySerLysSerGlyAsnThrAlaSerLeu 84  
284 CCATCTCTGGCTCCAGCGCTGAGGACGAGCTGATTACTGTGTCTCA 333  
|||||  
84 hrValSerGlyLeuGlnAlaGlnAspGluAlaAspTyrTyrCysSer 100  
334 TATACACCACTAGTACACTTTGTTATTCGAGAGGAGGACCGGTTGACCGT 383  
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101 TyrAlaGlySerAsnValPheGlyGlyThrLysLeuThrVa 117  
384 CCTAGGT 390  
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117 lLeuGly 119

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-139818

seq\_documentation\_block:  
; Sequence 139818, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; NUMBER OF SEQ ID NOS: 2001-02-22  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 139818  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-139818

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Ratio: 4.865 Gaps: 1  
Percent Similarity: 91.736 Percent Identity: 85.950

alignment\_block:  
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1 ThrGlnGlyThrGlySerTrpAlaGlnSerAlaLeuThrGlnProArgSe 17  
84 TGTCTCTGGTCTCCTGGACAGTCGGTCACATCTCTGCACGTGAACCA 133  
|||||  
17 rValSerGlySerProGlyGlnSerValThrIleSerCysThrGlyThrS 34  
134 GCGATGACGTTGGTGTATAAAC.....TATGTCTCTCTGGTACCAACAC 177  
|||||  
34 erSerAspValGlyGlyTyrAsnTyrAspTyrValSerTyrTyrGlnHis 50  
178 CACCAGGCAAGCCCCCAACTCATGATTATGATCGTCAAGCGGCGC 227  
|||||  
51 HisProGlyLysAlaProLysLeuMetIleTyrAspValSerLysArgPr 67  
228 CTGAGGGTCTCTGATCGCTTCTGGCTCCAACTCTGGCAACACGCGCT 277  
|||||  
67 oSerGlyValProAspArgPheSerGlySerLysSerGlyAsnThrAlaS 84  
278 CCTGACCATCTCTGGGCTCCAGGCTGAGGAGGCTGATTACTTACTGT 327  
|||||  
84 erLeuThrIleSerGlyLeuGlnAlaAspGluAlaAspTyrTyrCys 100  
328 TGTTCATATACACCACTAGTACACTTTGTTATTCGGAAGAGGACCGGTT 377  
|||||  
101 CysSerTyrAlaGlyAsnTyrIleLeuValPheGlyGlyThrLysLe 117  
378 GACCGTCTTAGGT 390  
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117 uThrValLeuGly 121

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-1654

seq\_documentation\_block:  
; Sequence 1654, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1654  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-1654

alignment\_scores:  
Quality: 538.50 Length: 131  
Ratio: 4.487 Gaps: 1  
Percent Similarity: 91.603 Percent Identity: 80.153

alignment\_block:  
US-09-019-441-1 x US-09-791-537-1654 ..

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101 GACAGTCGGTCACCATCTCTCGCACTGGGAACACGAGCATGACGTGTGGTGTG 150
34 lyGlnSerIleThrIleSerCysThrGlyThrSerSerAspValGlySer 50
151 TATAACTATGTCCTCGTACCAACACCCAGGCAAGCCGCCCAAACT 200
51 TyrAsnLeuValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67
201 CATGATTATGATCTCGCTAAGCGGGCCTCAGGGGTCTCTGATCGCTTCT 250
67 uMetIleTyrGluGlySerLysArgProSerGlyValSerAsnArgPheS 84
251 CTGGCTCAAGTCTGGCAACACGCGCTCCCTGCACATCTCTGGGCTCCAG 300
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301 GCTGAGCAGCAGGCTGATTATTACTGTGTTCATATACAAACAGTAGCAC 350
101 AlaGluAspGluAlaAspTyrTyrCysSerTyrAlaGlySerSerTh 117
351 TTTG 354
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117 rLeu 118
seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB pep: US-09-791-537
seq_documentation_block:
; Sequence 139139, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 139139
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-139139

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Quality: 527.00 Length: 131
Ratio: 4.504 Gaps: 1
Percent Similarity: 89.313 Percent Identity: 77.099

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1 MetaLtrpAlaLeuLeuLeuLeuLeuLeuLeuLeuLeuThrGlnGlyThrGly 17
51 CTGGGCTCAGTCTCCCCGACTCAGCTCCCTCTGTCTCTGGGTCTCCCTG 100
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValAsnGlySerProG 34
101 GACAGTCGGTCACCATCTCTCGCACTGGGAACACCCAGGCAAGCCGCCCAAACT 150
34 lyGlnLeuIleIleSerCysThrGlyThrSerSerAspIleGlyAsp 50
151 TATAACTATGTCCTCGTACCAACACCCAGGCAAGCCGCCCAAACT 200
51 TyrGlnTrpIleSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67

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Search time (sec): 70.150000

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/cgn2_6/pdata2/1aa/6B.COMB	pep:US-09-025-769B-19	+	502.00	980.74	3.4e-47
/cgn2_6/pdata2/1aa/6B.COMB	pep:US-08-918-148-79	+	497.00	963.02	1.5e-46
/cgn2_6/pdata2/1aa/6B.COMB	pep:US-08-958-201-14	+	466.00	910.02	3.0e-43
/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-938-201-12	+	462.00	902.15	8.2e-43
/cgn2_6/pdata2/1aa/6B.COMB	pep:US-09-025-769B-33	+	459.50	897.33	1.5e-42
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/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-646-360-153	+	395.50	772.01	1.6e-35
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/cgn2_6/pdata2/1aa/6B.COMB	pep:US-08-939-765-153	+	395.50	772.01	1.6e-35
/cgn2_6/pdata2/1aa/6B.COMB	pep:US-09-136-389-153	+	395.50	772.01	1.6e-35
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/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-665-202-43	+	376.00	732.99	2.2e-33
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/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-665-202-5	+	370.00	712.64	1.3e-32
/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-665-202-40	+	369.00	719.22	1.3e-32
/cgn2_6/pdata2/1aa/6B.COMB	pep:US-09-240-274-64	+	366.50	714.21	2.4e-32
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/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-665-202-42	+	362.00	705.45	7.4e-32
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/cgn2_6/pdata2/1aa/5B.COMB	pep:US-08-665-202-36	+	360.00	701.52	1.1e-31





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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-19

alignment_scores:
    Quality: 502.00      Length: 111
    Ratio: 4.781        Gaps: 0
    Percent Similarity: 94.595      Percent Identity: 86.486

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US-09-019-441-1 x US-09-025-769B-19 ..

Align seg 1/1 to: US-09-025-769B-19 from: 1 to: 112

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1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGTCAACATCTCTGCACCTGGAAACCAGCATGACGTTGGTGGTTATAACT 157
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17 rleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnT 34

158 ATGTCTCTCTGTACCAACACACACCAGCCAGCAAGCCCCCAAACTCATGATT 207
||||| |||||||
34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetIle 50

208 TATGATGTGCTAAGCGGGCTCTCAGGGTCTCTGTATCGTCTCTCTGGCTC 257
||||| |||||||
51 TyrAspValSerLysArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACGCGCTCCCTTGACCATCTCTGGGCTCCAGGCTGAGG 307
||||| |||||||
67 rlySerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTGTGTTTCATATACAAACCACTAGCACTTTGT 357
||||| |||||||
84 spGluAlaAspTyrTyrCysSerSerTyrAlaGlySerSerThrValVal 100

358 TTCGGAAGAGGACCGGTTGACCGTCTCTAGGT 390
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101 PheGlyGlyGlyThrLysLeuThrValLeuGly 111

seq_name: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:US-08-918-148-79

seq_documentation_block:
; Sequence 79, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: us/08/918,148A
; CURRENT FILING DATE: 1997-08-25

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; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,201
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/028,897
; FILING DATE: 21-OCT-1996
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: D12
; US-08-958-201-12

alignment_scores:
    Quality: 462.00      Length: 111
    Ratio: 4.574        Gaps: 0
    Percent Similarity: 90.991      Percent Identity: 79.279

alignment_block:
US-09-019-441-1 x US-08-958-201-12 ..

Align seg 1/1 to: US-08-958-201-12 from: 1 to: 111

58 CAGTCTGCCCGCAGCTCAGCCTCCCTCTGTGCTCTGGGTCTCTCTGGACAGTC 107
1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17
108 GGTCAACATCTCTGCATCGAACCAGCAGATGACGTTGGTGTATAACT 157
17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyTyTyLysr 34
158 ATGTCTCTCTGGTACCAACACACACCCAGGAAAGCCCCCAAACTCATGATT 207
34 yrValSerTrpTyGlnGlnHisProGlyLysAlaProLysLeuMetIle 50
208 TATGATCTCGCTAAGCGGCCCTCAGGGGCTCTGATCGCTCTCTCTGGCTC 257
51 PheGlyValSerAsnArgProSerGlyValProAsnArgPheSerGlySe 67
258 CAAGCTCGGCAACACGGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnValGlu 84
308 ACAGAGGCTGATTATTACTGTGTTCATATACACCAAGTAGCAGCTTTGTTA 357
84 spGluAlaAspTyTyCysSerSerLeuThrArgValThrValIle 100
358 TTGCGAAGAGGGACCGGTTGACCGTCTTAGGT 390
101 PheGlyGlyThrLysLeuThrValLeuGly 111

seq_name: /cqn2.6/ptodata/2/1aa/6B_COMB.pep:US-09-025-769B-33

seq_documentation_block:
; Sequence 33, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moronev, Simon

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; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-33

alignment_scores:
    Quality: 465.50      Length: 111
    Ratio: 4.564         Gaps: 1
    Percent Similarity: 91.892      Percent Identity: 81.982

alignment_block:
US-09-019-441-1 x US-09-025-769B-33  ..

Align seg 1/1 to: US-09-025-769B-33 from: 1 to: 110

58 CAGTCTGCCCGGACTCAGCCCTCCTGTGCTGTGGGTCTCTGGACAGTC 107
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   1 GlnSerAlaLeuThrGlnProAlaSerValSerGlySerProGlyGlnSe 17

108 GGCACACATCTCTGCACCTGGAACCGACGATGAGTGGTGGTTATAACT 157
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnT 34

158 ATGCTCTCTGGTACCAACACACCCAGCCAGCAAGCCCAAACTCATGATT 207
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetile 50

208 TATGATGTCGCTAAGCGGCTCTCAGGGGTCTCTGATCGCTCTCTGGCTC 257
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   51 TyrAspValSerAsnArgProSerGlyValSerAsnArgPheSerGlySe 67

258 CAAGTCTGGCAACACCGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84

308 ACGAGGCTGATTATTACTGTGTTGTTATATACACACCTAGACTTTGTTA 357
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   84 spGluAlaAspTyrTyrCysGlnGlnHisThrThrProPro...Val 99

358 TTCGGAAGAGGGACCGCGGTGACCGTCTCTAGGT 390
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seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pap:US-09-025-769B-53

seq_documentation_block:
; Sequence 53, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-53

alignment_scores:
    Quality: 465.50      Length: 111
    Ratio: 4.564         Gaps: 1
    Percent Similarity: 91.892      Percent Identity: 81.982

alignment_block:
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Align seg 1/1 to: US-09-025-769B-53 from: 1 to: 110

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108 GGCACACATCTCTGCACCTGGAACCGACGATGAGTGGTGGTTATAACT 157
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   17 rIleThrIleSerCysThrGlyThrSerSerAspValGlyGlyTyrAsnT 34

158 ATGCTCTCTGGTACCAACACACCCAGCCAGCAAGCCCAAACTCATGATT 207
   ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
   34 yrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLeuMetile 50
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208 TATGATCTCCTAAGCGGCTCAGGGCTCTCTGATCGCTTCTCTCTGCTC 257
51 TyrAspValSerAsnArgProSerGlyValSerAsnArgPheSerGlySe 67
258 CAAGTCTGGCAACAGCCCTCCCTGACCATCTCTGGGCTCCAGGCTGAGG 307
67 rLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluA 84
308 ACAGGCTGATATTACTGTGTTTCATATACAAACAGTAGCAGCTTTCTTA 357
84 spGluAlaAspTyrTyrCysGlnGlnHisTyrThrThrProPro...Val 99
358 TTCGAGAGAGGAGCCCGGTTGACCGTCTCTAGGT 390
100 PheGlyGlyThrLysLeuThrValLeuGly 110
seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pap:US-08-918-148-74
seq_documentation_block:
; Sequence 74, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 74
; LENGTH: 249
; TYPE: PRT
; ORGANISM: artificial
US-08-918-148-74
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Percent Similarity: 81.818 Percent Identity: 67.424
alignment_block:
US-09-019-441-1 x US-08-918-148-74
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116 MetValThrValSerSerGlyGlyGlySerGlyGlyGlySerGly 132
52 .....TGGCTCAGTCTGCCCGACTCAGCTCCCTCTGTCTGGGT 94
132 YGlyGlySerGlnSerValLeuThrGlnProAlaSerValSerGlyS 149
95 CTCCTGGACAGTGGTCACCATCTCTGCACTGGAAACGAGCATGAGTT 144
149 erProGlyGlnSerIleThrIleSerCysThrGlyThrSerGlyVal 165
145 GTTGGTTATTAACATATCTCTCTGGTACCAACACACCGAGCAAGCC 194
166 GlyGlyTyrAsnTyrValSerTyrGlnGlnHisProGlyLysAlaPr 182
195 CAAACTCATGATTATGATGTCGCTAAGCGGCTCAGGGGTCTCTGATC 244
182 oLysLeuLeuIleTyrGlyAsnSerAsnArgProSerGlyValProAsp 199
245 GCTTCTTGCTCAAGTCTGGCAACACAGCCCTCCCTGACCATCTCTGG 294
199 rgPheSerAlaSerLysSerGlyAsnThrAlaSerLeuThrIleSerGly 215
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295 CTCAGGCTGAGGACGAGGCTGATTACTGTGTTTCATATACAAACAGG 344
216 LeuGlnAlaGluAspGluAlaAspTyrPheCysSerThrTyrAlaProPr 232
345 TACACACTTTCTTATTTCGGAAGAGGGACCCGGTTGACCGTCTCTAGGT 390
232 oGlyIleIleMetPheGlyGlyThrLysLeuThrValLeuGly 247
seq_name: /cgn2_6/ptodata/2/1aa/6B_COMB.pap:US-09-049-672A-7
seq_documentation_block:
; Sequence 7, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/049,672A
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrione, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: ADRETUT05
; CLONE: 2492122
US-09-049-672A-7
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alignment_scores:
  Quality: 442.50      Length: 132
  Ratio: 3.916        Gaps: 3
Percent Similarity: 85.606 Percent Identity: 68.939
alignment_block:
US-09-019-441-1 x US-09-049-672A-7
Align seg 1/1 to: US-09-049-672A-7 from: 1 to: 236
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1 MetAlaTrpSerProLeuLeuThrLeuLeuAlaHisCysThrGlyLe 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51 CTGGGCTCAGTCTGCCCGACTCAGCTCCCTCTGTCTGGTCTCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 rTrpAlaGlnSerValLeuThrGlnProProSerValSerGlyAlaPro 34
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101 GACAGTGGTCCACCATCTCTGCACTGGAAACCCAGCAAGCCCAA 147
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34 LyGlnArgValThrIleSerCysThrGlySerSerSerAsnIleGlyAla 50
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148 GGTATTAATCTATGCTCTGCTGCTACCAACACCCAGCAAGCCCAA 197
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51 GlyTyrAsp...ValHisTrpTyrGlnGlnLeuProGlyThrAlaPro 66
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198 ACTCATGATTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
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66 sLeuLeuIleTyrGlySerArgAsnArgProSerGlyValProAspArg 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
248 TCTCTGGCTCCAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 297
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83 heSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleThrGlyLeu 99
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298 CAGGCTGAGGAGGAGGCTGATTACTTGTGTTTCATATACACCAAGT... 345
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100 GlnAlaGluAspGluAlaAspTyrTyrCysGlnSerTyrAspSerLe 116
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346 AGCATTCTGTTATTTCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 390
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116 uSerGlyValValPheGlyGlyGlyThrLysLeuThrValLeuGly 131
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seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:us-08-305-683A-4

seq_documentation_block:
; Sequence 4, Application US/08305683A
; Patent No. 5646041
; GENERAL INFORMATION:
; APPLICANT: HARFELDT, Elisabeth
; APPLICANT: LARE, Philip
; APPLICANT: NOTTAGE, Barbara
; APPLICANT: OSTBERG, Lars G.
; TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS AND CELL LINE PRODUCING THE SAME
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/305,683A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/759,279
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joe
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-005230
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-305-683A-4

alignment_scores:
  Quality: 436.50      Length: 132
  Ratio: 3.897        Gaps: 3
  Percent Similarity: 84.848      Percent Identity: 67.424

alignment_block:
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1 MetAlaTrpSerProLeuLeuThrLeuLeuAlaHisCysThrGlyLe 17
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51 CTGGGCTCAGTCTGCCCGACTCAGCTCCCTCTGTCTGGTCTCCTG 100
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17 rTrpAlaGlnSerValLeuThrGlnProProSerValSerGlyAlaPro 34
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101 GACAGTGGTCCACCATCTCTGCACTGGAAACCCAGCAAGCCCAA 147
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148 GGTATTAATCTATGCTCTGCTGCTACCAACACCCAGCAAGCCCAA 197
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51 GlyTyrAsp...ValHisTrpTyrGlnGlnLeuProGlyThrAlaPro 66
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198 ACTCATGATTTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 247
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66 sLeuLeuIleTyrGlySerArgAsnArgProSerGlyValProAspArg 83
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248 TCTCTGGCTCCAAGTCTGGCAACAGCGCTCCCTGACCATCTCTGGGCTC 297
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83 heSerGlySerLysSerGlyThrSerAlaSerLeuAlaIleThrGlyLeu 99
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100 GlnAlaGluAspGluAlaAspTyrTyrCysGlnSerTyrAspSerGlyLe 116
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346 AGCATTCTGTTATTTCGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGT 390
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116 uSerGlySerIlePheGlyGlyGlyThrLysLeuThrValLeuGly 131
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seq_documentation_block:
; Sequence 68, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: SORTING METHOD FOR PRODUCTION THEREOF
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain R01
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US-09-240-274-68

alignment\_scores:  
Quality: 421.50 Length: 106  
Ratio: 4.301 Gaps: 1  
Percent Similarity: 92.453 Percent Identity: 75.472

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US-09-019-441-1 x US-09-240-274-68 ..

Align seg 1/1 to: US-09-240-274-68 from: 1 to: 108

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170 ACCAACACCCAGGCAAGCCCAACATCATGATTATGATGTCGCT 219
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37 yrGlnGlnHisProGlyLysAlaProLysLeuThrHisGluGlyThr 53
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54 LysArgProSerGlyValProAspArgPheSerGlySerLysSerGlyAs 70
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270 CACGGCTCCTCAGCATCTCTGGCTCCAGGCTGAGGACGAGCTGATT 319
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70 nThrAlaSerLeuThrValSerGlyLeuGlnAlaGluAspGluAlaAsp 87
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320 ATTACTGTGTTCATATACACACAGTAGCACTTTGTTATTTCGGAAGAGG 369
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87 yrTyCysSerSerPheAlaGlyAsnSer...ValIlePheGlyGly 102
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seq\_documentation\_block:  
; Sequence 69, Application US/09240274  
; Patent No. 6255455  
; GENERAL INFORMATION:  
; APPLICANT: Siegel, Donald L.  
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL  
; FILE REFERENCE: 09596-42U2  
; CURRENT APPLICATION NUMBER: US/09/240,274  
; CURRENT FILING DATE: 1999-01-29  
; EARLIER APPLICATION NUMBER: 60/081,380  
; EARLIER FILING DATE: 1998-04-10  
; EARLIER APPLICATION NUMBER: 60/028,550  
; EARLIER FILING DATE: 1996-10-11  
; NUMBER OF SEQ ID NOS: 224  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 69  
; LENGTH: 104  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: anti-Rh(D) chain S01  
US-09-240-274-69

alignment\_scores:  
Quality: 413.50 Length: 106  
Ratio: 4.353 Gaps: 2  
Percent Similarity: 89.623 Percent Identity: 76.415

alignment\_block:

US-09-019-441-1 x US-09-240-274-69 ..

Align seg 1/1 to: US-09-240-274-69 from: 1 to: 104

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70 ACTCAGCCTCCTCTGTGCTCTGGTCTCTCCAGCAGTCGGTCACCATCTC 119
|||||
4 ThrGlnProProSerValSerGlySerProGlyGlnSerIleThrIleSe 20
|||||
120 CTGCACCTGGAAACACGAGCATGACGTTGGTGTATTAACATATCTCTCGGT 169
|||||
20 rCysSer.....AspValGlyAsnTyrAsnLeuValSerTrp 33
|||||
170 ACCAACACCCAGGCAAGCCCAACATCATGATTATGATGTCGCT 219
|||||
33 yrGlnGlnTyrProGlyLysAlaProLysLeuIleTyrGluGlySer 49
|||||
220 AAGCGGGCCTCAGGGGCTCTGTATCGCTTCTCTGGCTCCAAAGTCGGCAA 269
|||||
50 LysArgProSerGlyValSerSerArgPheSerGlySerArgSerGlyAs 66
|||||
270 CACGGCTCCTCAGCATCTCTGGCTCCAGGCTGAGGACGAGCTGATT 319
|||||
66 nThrAlaSerLeuThrIleSerGlyLeuGlnAlaGluAspGluAlaAsp 83
|||||
320 ATTACTGTGTTCATATACACACAGTAGCACTTTGTTATTTCGGAAGAGG 369
|||||
83 yrHisCysSerTyrAlaIleSerSerArg...IlePheGlyGly 98
|||||
370 ACCCGGTGACCGTCCTA 387
|||||
99 ThrLysLeuThrValLeu 104
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seq\_name: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:US-08-652-816A-15

seq\_documentation\_block:  
; Sequence 15, Application US/08652816A  
; Patent No. 5872215  
; GENERAL INFORMATION:  
; APPLICANT: Osbourn, JK  
; APPLICANT: Allen, DJ  
; APPLICANT: McCafferty, JG  
; TITLE OF INVENTION: Specific binding members, materials and  
; TITLE OF INVENTION: methods.  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 6300 Sears Tower, 233 South Wacker Drive  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States of America  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/652,816A  
; FILING DATE: 23-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.4  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9125579.8  
; FILING DATE: 02-DEC-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206318.9  
; FILING DATE: 24-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9206372.6  
; FILING DATE: 23-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: GB 9525004.9



122 yGlyGlyThrArgLeuThrValLeuGly 131

---





100 LeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAlaArg.. 115  
357 TTGGGCCCAATAGCTGGAACAAG..... 381  
116 .....ValThrGlySerThrPheTrpSerGlyTyrTyrThrArgG 129

382 .....CTAGGCTTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 423  
129 lyTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 145  
seq\_name: pir2:SI3519

## seq\_documentation\_block:

Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 25-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: SI3519  
R:Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.  
Nucleic Acids Res. 19, 673, 1991  
A:Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with x-linked  
A:Reference number: SI3519; MUID:91187691  
A:Accession: SI3519  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-147 <NOR>  
A:Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:41-125/Domain: immunoglobulin homology <IMM>

## alignment\_scores:

Quality: 557.50 Length: 144  
Ratio: 4.460 Gaps: 4  
Percent Similarity: 86.806 Percent Identity: 79.167

## alignment\_block:

US-09-019-441-2 x SI3519 ..

Align seg 1/1 to: SI3519 from: 1 to: 147

1 ATGAACACCTGTGGTCTTCTCCTCCTCGTGGCCAGCTCCAGATGGT 50  
8 MetlyshisLeutrrpPhePheLeuLeuValAlaAlaProArgTrpVa 24  
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTT 100  
24 LLeuSerGlnLeuGlnLeuGlnGluSerGlyProGlyLeuVallysp 41  
101 CGGAGACCTGTCCCTCACCTGGCTCTCTGTGGCTCTGTGAGCAGT 150  
41 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerileSer 57  
151 AGTAAC...TGGTGGACCTGGATCCGCCAGCCCCAGGAGGACTGGA 197  
58 SerSerTyrTrpGlyTrpGlyTrpIleArgGlnProGlyLysGlyLeu 74  
198 GTGGATTGGACGTATCTCTGGTAGTGTGGGGCCACCACTACAACCGT 247  
74 utPleGlySerileTyrTyrSer...GlySerThrTyrTyrAsnPro 90  
248 CCTCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAAAGAACCA 297  
90 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGln 106  
298 TCCTTGAACTGAACTGTGTGACCGCGGACACGCGCTGTATTACTG 347  
107 SerLeuLysSerSerValThrAlaAlaAspThrAlaValTyrTyrCy 123  
348 TGCACAGAGAT.....TGGGCCCAAAATAGCTGGAACAACCTAGGCT 391  
123 sAlaArgProLeuLeuTrp.....PheGlyGluLeuPheAspTyrT 137

392 GGGCCAGGAGTCTGTGTACCGCTCCTCTCA 423  
137 rpGlyGlnGlyThrLeuValThrValSerSer 147

seq\_name: pir2:I37782

## seq\_documentation\_block:

Ig variable region (VDU) (clone T23-9) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 16-Feb-1996 #sequence\_revision 13-Mar-1997 #text\_change 23-Jul-1999  
C:Accession: I37782; S25476  
R:Demaision, C.; Chastagner, P.; Theze, J.; Zouali, M.  
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994  
A:Title: Somatic diversification in the heavy chain variable region genes expressed b  
A:Reference number: A36876; MUID:94119917  
A:Accession: I37782  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <RES>  
A:Cross-references: EMBL:X67906; NID:g33582; PIDN:CAA48104.1; PID:g33583  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:46-128/Domain: immunoglobulin homology <IMM>

## alignment\_scores:

Quality: 556.50 Length: 145  
Ratio: 4.417 Gaps: 4  
Percent Similarity: 86.897 Percent Identity: 77.931

## alignment\_block:

US-09-019-441-2 x I37782 ..

Align seg 1/1 to: I37782 from: 1 to: 140

1 ATGAACACCTGTGGTCTTCTCCTCCTCGTGGCCAGCTCCAGATGGT 50  
1 MetlyshisLeutrrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCCTT 100  
17 LLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuVallysp 34  
101 CGGAGACCTGTCCCTCACCTGGCTCTCTGTGGCTCTGTGAGCAGT 150  
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerile...Ser 49  
151 AGTAACCTGGTGGACCTGGATCCGCCAGCCCCAGGAGGACTGGAGTG 200  
50 SerTyrTyrTrpSerTrpIleArgGlnProGlyLysGlyLeuGluTr 66  
201 GATTGGACGTATCTCTGGTAGTGTGGGGCCACCACTACAACCCGTC 250  
66 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProser 82  
251 TCAGAGTCGAGTCATCATTTCAAGACACAGCTCCAAAGAACCACTCC 300  
82 eulySerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 98  
301 CTGAACCTGAACTCTGTGACCGCGGACACGCGCTGTATTACTGTGC 350  
99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCys 115  
351 CAGA.....GATTGGGCCCAAAATAGCTGGAACAACCTAGGCT 388  
115 aa9HisAsnSerSerTrp.....TyrGlyArgTyrPheAspT 129  
389 TCTGGGCCAGGAGTCTGTGTACCGCTCCTCTCA 423  
129 yrrpGlyGlnGlyThrLeuValThrValSerSer 140

seq\_name: pir2:S31586

seq\_documentation\_block:

Ig heavy chain V region - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
 C/Accession: S31586  
 R/Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
 submitted to the EMBL Data Library, June 1992  
 A/Description: Mechanisms that generate human immunoglobulin diversity operate from the  
 A/Reference number: S31585  
 A/Accession: S31586  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-139 <CUI>  
 A/Cross-references: EMBL:Z14196; PID:g30978; PID:CAA78565.1; PID:g30979  
 C/Superfamily: immunoglobulin V region; immunoglobulin homology  
 C/Keywords: heterotetramer; immunoglobulin  
 F/34-116/Domain: immunoglobulin homology <IMM>

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alignment_scores:
  Quality: 553.00      Length: 141
  Ratio: 4.424        Gaps: 2
  Percent Similarity: 88.652  Percent Identity: 78.014
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alignment\_block:  
US-09-019-441-2 x S31586

Align seg 1/1 to: S31586 from: 1 to: 139

1 ATGAACACCTGTGGTCTTCTCTCTCTGGTGGCAGCTCCCAAGATGGGT 50  
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVal 17  
51 CCTGTCCCACTGCAGCTGCAGGAGTCGGGCCCAAGGATGGTCAAGCCCT 100  
17 IleuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCGCTGCCCTCACCCTGGCTGTCTCTGGTGGCTCTGTGCAGCAT 150  
|||||  
34 erGLuThrLeuSerLeuThrCysThrValSerGLvGLvSsrIle...Ser 49

151 AGTAACTGGTGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG 200  
||| :|||:::|||:|||:||| ||||| ||||| |||||  
50 SerTVrVTrpSerTrpIleAraGlnProAla[ac]vIvsG[V]enGluTr 66

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCC 250  
|||||  
66 pIleGlvArgIleTyrThrSer...G|vSerThrAsnTyrAsnProSerI 82

251 TCAAGAGTCGAGTCATCATTTCAAGAAGACACGTTCCAAGAACCGAGTTCTCC 300  
|||||  
||||| : : : :  
82 enlVsSerArgValThrMetSerValAspThrSerIleuSerClnpPhoSer 08

301 CTGAACCTGAACTCTGTGACCGCGCGGCAGCAGCGCGTGTATTACTGTGC 350  
|||||  
99 LeifLvsLeifSerSerValThrAlaAlaadenBrAlaValTurTurCucAl 115

351 CAGAGATTGGGCCCAAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGG 400

401 GAGTCTGGTCACCGTCTCCTCA 423  
|||||:|||||||

seq\_name: pir2:S31676

```
seq_documentation_block:
  Ig heavy chain V region - human (fragment)
  C:Species: Homo sapiens (man)
  C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
  C:Accession: S31676
  R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
  Submitted to the EMBL Data Library, June 1992
```

A:Description: Mechanisms that generate human immunoglobulin diversity operate from t  
A:Reference number: S31585  
A:Accession: S31676  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-137 <CUI>  
A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:		
Quality:	552.00	Length: 141
Ratio:	4.452	Gaps: 3
Percent Similarity:	87.943	Percent Identity: 78.723

alignment\_block:  
US-09-019-441-2 x S31676

Align seq 1/1 to: S31676 from: 1 to: 137

1 ATGAAACACCTGTGGTTCTTCTCTCTCTGGTGGCAGCTCCCAGATGGGT 50  
|||||  
1 MetLysHisLeuTrpphepheLeuLeuLeuValAlaAlaProArgTrpVa 17

51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCCAGGAGTGGTGAGGCCTT 100  
|||||{}:|||||{}:|||||{}:|||||{}:|||||{}:  
17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCCCTGTCCTCACCTGCCTGTCTCTGGTGGCTCTGTCAGCAGT 150  
 |||||  
 34 erGluThrIeuSerIeuThrCysThrValSerGlyGlySerIle...Ser 49  
 |||||

151 AGTAACTGGTGACCTGGATCCGCCAGCCCCCAGGAGGACTGGAGTG 200  
||| :|||:::||||| ||||| ||||| ||||| |||||  
50 SerTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr 66

201 GATTGGACGTATCTCTGGTAGTGTGGGGCCACCAACTACACCCCGTCC 250  
|||||  
66 pIleGIVArIleTvrThrSer...GIVSerThrAsnTvrAsnProSerL 82  
|||||

251 TCACAGGTCGAGTCAATCATTTTCACAAAGACACGTCCACGAACCAGTTCTCC 300  
|||||  
82 euLvsSerAraVaThrMetSerValAsnThrSerIvcaAsnGlnPheSer 98  
||||| :||| |||||

301 CTGAACCTGAACTCTGTGACCGCCGGACACGGCCGTGTATTACTGTGC 350  
|||:::||:::||:::||:::||:::||  
90 LeuIvsiLeuSerSerValThrAlaAlaLeuThrAlaValTyrMetCysAl 115

351 CAGAGATTGGGCCCAATAGCTGGAACAACGCTAGGCTTCTGGGGCCAGG 400  
||||| :|||  
||||| :|||  
365 AAGCGAAlaDeoIouMotmyrCl:  
||||| :|||  
380 MetAcvAlaMetmyrCl:CleC 120

401 GAGTCTGGTCACCGTCTCCTCA 423  
||:: |||||||  
20 |ambhtvta16mbhtv16GenG 127

seq\_name: pir2:s31696

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seq_documentation_block:
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-
C:Accession: S31696
```

C;Accession: S31696  
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.  
submitted to the EMBL Data Library, June 1992  
A;Description: Mechanisms that generate human immunoglobulin diversity operate from t  
A;Reference number: S31585

A;Reference number: S31696  
A;Accession: S31696  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-139 <CUI>



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US-09-019-441-2 x S31512
Align seg 1/1 to: S31512 from: 1 to: 155

1 ATGAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGGT 50
14 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 30
51 CCTGTCCAGCTGCAGCTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100
30 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 47
101 CGGAGACCTGTCTCTCTCACCTGCCTCTCTCTGTGGTCTGTGCAGCT 150
47 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 62
151 AGTAACCTGGTGGACCTGCAGTCCGCCAGCCAGGAGGAGGAGTGGAGTG 200
63 SerTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 79
201 GATTGGAGCTATCTCTGTGTAGTGGTGGGGCCAGCACTACAACCCGTCC 250
79 pIleGlyTyrIleTyrTrpThrGlySerAlaThr...TyrAsnProI 95
251 TCAAGAGTCGAGTCATCATTTCAACACACAGCTCCAAGAACCACTTCTCC 300
95 leLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 111
301 CTGAACCTGAACCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGC 350
112 LeuLysValSerSerValThrAlaAlaAspThrAlaValTyrCysAl 128
351 CAGA.....GATTGGGCCCAATAGCTGGACACACGCTAG 385
128 aArgGlyGlyGlyIleSerSerTrpTyrValTyrGly.....MetA 143
386 GCTTCTGGCGCAGGAGTCTGTGCTACCGCTCTCTCTCA 423
143 spValTrpGlyGlnGlyThrThrValThrValSerSer 155

seq_name: p1r2:A49045
seq_documentation_block:
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (nan)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Pillier, F.; Rassenti, L.Z.; Labaune, S.; Silverma
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A:Reference number: A49045; MUID:92324290
A:Accession: A49045
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GRI>
A:Cross-references: GB:S39381; NID:g250899; PIDN:AAB22441.1; PID:g250900
A>Note: sequence extracted from NCBI backbone (NCBI:108088, NCBI:108089)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 530.50 Length: 142
Ratio: 4.278 Gaps: 3
Percent Similarity: 87.324 Percent Identity: 75.352

alignment_block:
US-09-019-441-2 x A49045
Align seg 1/1 to: A49045 from: 1 to: 140

1 ATGAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGGT 50
```

```
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGCTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100
17 lLeuSerGlnValGlnLeuGlnGluTrpGlyAlaGlyLeuLeuLysPro 34
101 CGGAGACCTGTCTCTCTCACCTGCCTCTCTCTGTGGTCTGTGCAGCT 150
34 erGluThrLeuSerLeuThrCysAlaValTyrGlyGlySerPhe...Ser 49
151 AGTAACCTGGTGGACCTGCAGTCCGCCAGCCAGGAGGAGGAGTGGAGTG 200
50 GlyTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66
201 GATTGGAGCTATCTCTGTGTAGTGGTGGGGCCAGCACTACAACCCGTCC 250
66 pIleGlyGlyIleAsnHisSer...GlySerThrAsnTyrAsnProSerL 82
251 TCAAGAGTCGAGTCATCATTTCAACACACAGCTCCAAGAACCACTTCTCC 300
82 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 98
301 CTGAACCTGAACCTGTGACCGCGCGGACACGCGCGTGTATTACTGTGC 350
99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAl 115
351 CAGA...GATTGGGCCCAATAGCTGGACACACGCTAGGCTTCTGGGGCC 397
115 aArgGlyGlyPheAlaAlaThrIleValGluSerPheAspTyrTrpGlyG 132
398 AGGAGTCCTGTGGTCCACGCTCTCTCA 423
132 lGlyThrLeuValThrValSerSer 140

seq_name: p1r2:S09711
seq_documentation_block:
Ig heavy chain V region - human
C:Species: Homo sapiens (nan)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C:Accession: S09711
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
Biochem. J. 268, 135-140, 1990
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domain
A:Reference number: S09710; MUID:90262535
A:Accession: S09711
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-146 <HUG>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-118/Domain: immunoglobulin homology <IMM>

alignment_scores:
Quality: 522.50 Length: 149
Ratio: 4.147 Gaps: 4
Percent Similarity: 84.564 Percent Identity: 71.812

alignment_block:
US-09-019-441-2 x S09711
Align seg 1/1 to: S09711 from: 1 to: 146

1 ATGAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGGT 50
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpCy 17
51 CCTGTCCAGCTGCAGCTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100
17 sLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 34
```

```
101 CGGAGACCTCTCCCTCACCTCCGCTCTCTCTGTGGCTCTGTGACGAGT 150
|||||
34 erGluThrLeuSerValThrCysThrValSerGlyGlySerValSerSer 50
|||||
151 AGTAAC...TGGTGACCTGGATCGGCGGAGCCGCCAGGAGGAGGACTGGA 197
|||||
51 SerGlyLeuTyrrpSerTrpIleArgGlnProProGlyLysGlyProGln 67
|||||
198 GTGATTGGAGCTATCTCTGTGTGGTGGGCGCCACCACTACAAACCGT 247
|||||
67 uTrpIleGlyTyrrpIleTyrrpSer...GlySerThrAsnThrAsnProS 83
|||||
248 CCCTCAAGAGTCGAGTCATCTTCAACAGACAGCTCCAAGAACAGTTC 297
|||||
83 erLeuArgSerArgValThrIleSerValAspThrSerLysAsnGlnPhe 99
|||||
298 TCCTGAACCTGAACTCTGTGACCGCGGACAGCGCTCCAAGAACAGTTC 347
|||||
100 SerLeuLysLeuGlySerValThrAlaAlaAspThrAlaValTyrrCy 116
|||||
348 TGCCAGAGATTGGGCGCCAAATAGCTGGAACAACGCTAGGC..... 387
|||||
116 sAlaArg.....ValLeuValSerArgThrSerIleSerGlnTyrrSert 131
|||||
388 .....TTCTGGGCGCAGGAGTCTCTGTGTCACCGCTCTCTCTCA 423
|||||
131 yrTyrrMetAspValTrpGlyLysGlyThrValThrValSerSer 146
|||||
```

seq\_name: pir2:S09710

seq\_documentation\_block:

Ig heavy chain V region - human  
N:Alternate names: Ig heavy chain V region (DP-66)  
C:Species: Homo sapiens (man)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S09710  
R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.  
Biochem. J. 268, 135-140, 1990  
A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of  
A:Reference number: S09710; MUID:90262535

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-146 <HUG>

A:Cross-references: GB:X52110; NID:g31447; PIDN:CAA36344.1; PID:g31448

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-118/Domain: immunoglobulin homology <IMM>

alignment\_scores:

Quality:	520.50	Length:	153
Ratio:	4.232	Gaps:	4
Percent Similarity:	80.392	Percent Identity:	69.935

alignment\_block:

US-09-019-441-2 x S09710 ..

Align seg 1/1 to: S09710 from: 1 to: 146

```
1 ATGAACACCTGTGGTTCCTCTCTCTCTGTGGTGGGAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
|||||
51 CTTGTCCACGCTCAGCTCAGAGTCGAGGAGTGGGCGGAGGAGTGGTGAAGCCTT 100
|||||
17 lLeuSerGlnLeuArgLeuGlnGlnSerGlyProGlyLeuValLysProS 34
|||||
101 CGGAGACCTGTCCCTCACCTCCGCTCTCTGTGTCACCGCTCTGTCAGCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerValSerSer 50
|||||
151 AGTAAC...TGGTGGACCTGGATCCGCGGAGCCCGGAGGAGGAGGACTGGA 197
|||||
```

```
51 GlyGlyLeuTyrrpGlyTrpValArgGlnProProGlyLysGlyLeuGl 67
|||||
198 GTGATTGGAGCTATCTCTGTGTGGTGGGCGCCACCACTACAAACCGT 247
|||||
67 uTrpIleGlySerIlePheTyrrSer...GlySerThrTyrrAsnProS 83
|||||
248 CCCTCAAGAGTCGAGTCATCTTCAACAGACAGCTCCAAGAACAGTTC 297
|||||
83 erLeuLysSerArgValThrIleSerValAspThrLeuLysAsnAsnPhe 99
|||||
298 TCCTGAACCTGAACTCTGTGACCGCGGACAGCGCTCCAAGAACAGTTC 347
|||||
100 SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrrCy 116
|||||
348 TGCCAGAGAT.....TGGGCGCC 364
|||||
116 sThrArgProGlyTyrrGlyAspThrSerValArgLysArgValTrp.... 131
|||||
365 AAATAGCTGGAACAACAGCTAGGCTTCTGGGCGCAGGAGTCTCTGTGTCACC 414
|||||
132 .....AsnMetAspLeuTrpGlyGlnGlyThrValThr 143
|||||
415 GTCTCTCTCA 423
|||||
144 ValSerSer 146
|||||
```

seq\_name: pir2:A26340

seq\_documentation\_block:

Ig heavy chain precursor V-II region (71-2) - human  
N:Alternate names: Ig heavy chain V region (DP-66)  
C:Species: Homo sapiens (man)

C:Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
C:Accession: A26340; S26901

R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
J. Mol. Biol. 190, 529-541, 1986

A:Title: Organization and evolution of variable region genes of the human immunoglobulin

A:Reference number: A26340; MUID:87061007

A:Accession: A26340

A:Molecule type: DNA

A:Residues: 1-118 <KOD>

A:Cross-references: GB:M29811; NID:g185597; PIDN:AAC99493.1; PID:g553419

A:Note: the authors translated the codon GAG for residue 25 as Gln

R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.

J. Mol. Biol. 227, 776-798, 1992

A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o

A:Reference number: S26885; MUID:93021117

A:Accession: S26901

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 20-118 <TOM>

A:Cross-references: EMBL:Z12366; NID:g32950; PIDN:CAA78236.1; PID:g32951

C:Genetics:

A:Introns: 16/1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-118/Product: Ig heavy chain V-II region 71-2 #status predicted <MAT>

F:34-118/Domain: immunoglobulin homology <IMM>

alignment\_scores:

Quality:	518.00	Length:	119
Ratio:	4.667	Gaps:	2
Percent Similarity:	93.277	Percent Identity:	86.555

alignment\_block:

US-09-019-441-2 x A26340 ..

Align seg 1/1 to: A26340 from: 1 to: 118

```
1 ATGAACACCTGTGGTTCCTCTCTCTCTGTGGTGGGAGCTCCAGATGGGT 50
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```

1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
 51 CCGTGTCCACCTGCAGTCGAGAGTCGGCCCGAGAGTGGTGAAGCCTT 100  
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34  
 101 CGGAGACCCCTGTCCTCCACCTGCCTGCTCTCTGGTGGCTGTGCACAGT 150  
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerValSerSer 50  
 151 ...AGTAACTGGTGGACCTGCATCCGCCAGCCCGCCAGGAGGACTGGA 197  
 51 GlySerTyrtTrpSerTrpPheArgGlnProProGlyLysGlyLeuG 67  
 198 GTGGATTGGACGATCTCTCGGTAGTGGTGGGCCACCACTACAACCGT 247  
 67 uTrpPheGlyTyrtTrpSer...GlySerThrAsnTyrtAsnProS 83  
 248 CCCTCAAGAGTCAGTCATCATTTTCAACAGACACAGTCCCAAGAACCACTTC 297  
 83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe 99  
 298 TCCTGAACCTGAACCTGTGTACCGCGCGGACACAGCCCGCTGTATTACTG 347  
 100 SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrtCy 116  
 348 TGCAGA 354  
 116 sAlaArg 118  
 seq\_name: pir2:B26340

seq\_documentation\_block:  
 Ig heavy chain precursor V-II region (71-4) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 05-Jun-1988 #sequence\_revision 30-Jun-1991 #text\_change 23-Jul-1999  
 R:Kodaira, M.; Kinashi, T.; Umemura, I.; Matsuda, F.; Noma, T.; Ono, Y.; Honjo, T.  
 J. Mol. Biol. 190, 529-541, 1986  
 A:Title: Organization and evolution of variable region genes of the human immunoglobulin  
 A:Reference number: A26340; MUID:87061007  
 A:Accession: B26340  
 A:Molecule type: DNA  
 A:Residues: 1-116 <KOD>  
 A:Cross-references: GB:X05711; NID:g33502; PIDN:CAA29183.1; PID:g296660  
 A:Note: the authors translated the codon GAG for residue 25 as Gln  
 C:Genetics: 16/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-116/Product: Ig heavy chain V region 71-4 #status predicted <MAT>  
 F:34-116/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
 Quality: 514.00 Length: 118  
 Ratio: 4.673 Gaps: 2  
 Percent Similarity: 93.220 Percent Identity: 86.441  
 alignment\_block:  
 US-09-019-441-2 x B26340 ..  
 Align seg 1/1 to: B26340 from: 1 to: 116  
 1 ATGAACACCTGTGGTTCTTCCTCCTCGTGGTGGCAGCTCCACAGATGGGT 50  
 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
 51 CCGTGTCCACCTGCAGTCGAGAGTCGGCCCGAGAGTGGTGAAGCCTT 100  
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34

101 CGGAGACCTGTCCCTCACCTGCCTGCTCTCTGGTGGCTGTGCACAGT 150  
 34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerVal...Ser 49  
 151 AGTAACTGGTGGACCTGCATCCGCCAGCCCGCCAGGAGGACTGGAGTG 200  
 50 SerTyrtTrpSerTrpPheArgGlnProProGlyLysGlyLeuGluTr 66  
 201 GATTGACGATATCTCTGGTAGTGGTGGGCCACCACTACAACCCGTCCTC 250  
 66 pLleGlyTyrtIleTyrtSer...GlySerThrAsnTyrtAsnProSerL 82  
 251 TCAAGAGTCGAGTCATCATTTTCAACAGACACAGTCCCAAGAACCACTTC 300  
 82 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 98  
 301 CTGAACCTGAACCTGTGTACCGCGCGGACACAGCCCGCTGTATTACTGTGC 350  
 99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrtCysAl 115  
 351 CAGA 354  
 115 aArg 116  
 seq\_name: pir2:E34964

seq\_documentation\_block:  
 Ig heavy chain precursor V-IV region (Ab26) - human  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Sep-1990 #sequence\_revision 23-Nov-1991 #text\_change 16-Aug-1996  
 C:Accession: E34964  
 R:Sanz, I.; Casali, P.; Thomas, J.W.; Notkins, A.L.; Capra, J.D.  
 J. Immunol. 142, 4054-4061, 1989  
 A:Title: Nucleotide sequences of eight human natural autoantibody V-H regions reveals  
 A:Reference number: A92830; MUID:89235232  
 A:Accession: E34964  
 A:Molecule type: mRNA  
 A:Residues: 1-117 <SAN>  
 A:Cross-references: GB:M26997  
 A:Note: the authors translated the codon GCT for residue 42 as Thr  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
 Quality: 511.50 Length: 117  
 Ratio: 4.693 Gaps: 1  
 Percent Similarity: 93.162 Percent Identity: 84.615  
 alignment\_block:  
 US-09-019-441-2 x E34964 ..  
 Align seg 1/1 to: E34964 from: 1 to: 117  
 1 ATGAACACCTGTGGTTCTTCCTCCTCGTGGTGGCAGCTCCACAGATGGGT 50  
 1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
 51 CCGTGTCCACCTGCAGTCGAGAGTCGGCCCGAGAGTGGTGAAGCCTT 100  
 17 lLeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34  
 101 CGGAGACCTGTCCCTCACCTGCCTGCTCTCTGGTGGCTGTGCACAGT 150  
 34 erGlnThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerSer 50  
 151 AGTAACTGGTGGACCTGCATCCGCCAGCCCGCCAGGAGGACTGGAGTG 200  
 51 GlyAspTyrtTrpSerTrpPheArgGlnHisProGlyLysGlyLeuGluTr 67  
 201 GATTGACGATATCTCTGGTAGTGGTGGGCCACCACTACAACCCGTCCTC 250





OM of: US-09-019-441-2 to: SwissProt\_40.\* out\_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+np2p.model -DEV=xlp  
-O=/cn2\_1/USPTO\_spool/US09019441/runat\_23092002\_095259\_6394/app\_query.fasta\_1.1860  
-DB=SwissProt\_40 -Qfmt=fastan -SUFFIX=rsp -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPL=0.000 -LOOPEXT=0.000  
-OGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-RGAPOP=6.000 -RGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR\_SCORE=pct  
-THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09019441 -CGN1\_1.91 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-019-441-2  
Query length: 423  
Database: SwissProt\_40.\*  
Database sequences: 105224  
Database length: 38719550  
Search time (sec): 62.410000

score\_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SwissProt_40:HV21_HUMAN	+	444.50	702.54	1.3e-31	146   P06331 homo sapiens (human)
SwissProt_40:HV2F_HUMAN	+	381.50	604.17	4.6e-26	129   P01824 homo sapiens (human)
SwissProt_40:HV46_MOUSE	+	378.00	598.14	9.3e-26	137   P01822 mus musculus (mouse)
SwissProt_40:HV2G_HUMAN	+	368.50	584.48	6.3e-25	116   P01825 homo sapiens (human)
SwissProt_40:HV60_MOUSE	+	367.00	582.18	8.9e-25	116   P18531 mus musculus (mouse)
SwissProt_40:HV02_XENLA	+	354.50	561.19	1.1e-23	135   P20957 xenopus laevis (afri
SwissProt_40:HV47_MOUSE	+	352.50	559.52	1.6e-23	113   P01823 mus musculus (mouse)
SwissProt_40:HV43_MOUSE	+	345.00	547.47	7.3e-23	116   P18532 mus musculus (mouse)
SwissProt_40:HV62_MOUSE	+	344.50	544.87	8.2e-23	144   P01819 mus musculus (mouse)
SwissProt_40:HV44_MOUSE	+	336.50	533.98	4.1e-22	117   P18533 mus musculus (mouse)
SwissProt_40:HV45_MOUSE	+	311.00	493.89	7.1e-20	115   P01820 mus musculus (mouse)
SwissProt_40:HV2H_HUMAN	+	305.00	484.35	2.4e-19	116   P01821 mus musculus (mouse)
SwissProt_40:HV40_MOUSE	+	303.00	480.98	2.4e-19	147   P04438 homo sapiens (human)
SwissProt_40:HV37_MOUSE	+	298.00	473.09	3.6e-19	119   P01810 mus musculus (mouse)
SwissProt_40:HV01_XENLA	+	298.00	471.97	9.9e-19	119   P01807 mus musculus (mouse)
SwissProt_40:HV3B_HUMAN	+	295.00	468.72	1.0e-18	136   P20956 xenopus laevis (afri
SwissProt_40:HV3C_HUMAN	+	293.50	466.13	2.9e-18	114   P01763 homo sapiens (human)
SwissProt_40:HV05_CARAU	+	293.00	465.41	2.7e-18	116   P19181 carassius auratus (gc
SwissProt_40:HV38_MOUSE	+	293.00	465.20	2.7e-18	119   P01808 mus musculus (mouse)
SwissProt_40:HV36_HUMAN	+	293.00	464.99	2.7e-18	122   P01768 homo sapiens (human)
SwissProt_40:HV41_MOUSE	+	292.50	464.55	3.0e-18	117   P01811 mus musculus (mouse)
SwissProt_40:HV01_RAT	+	288.50	456.62	6.9e-18	142   P01805 rattus norvegicus (rat)
SwissProt_40:HV2B_HUMAN	+	287.00	455.66	9.2e-18	120   P01815 homo sapiens (human)
SwissProt_40:HV3U_HUMAN	+	286.50	454.80	1.0e-17	121   P01771 homo sapiens (human)
SwissProt_40:HV2C_HUMAN	+	285.50	453.37	1.2e-17	119   P01816 homo sapiens (human)
SwissProt_40:HV07_MOUSE	+	285.00	451.28	1.4e-17	139   P01751 mus musculus (mouse)
SwissProt_40:HV3T_HUMAN	+	283.00	449.64	2.1e-17	116   P01781 homo sapiens (human)
SwissProt_40:HV03_CAICR	+	282.50	448.77	2.3e-17	117   P03982 caiman crocodilus (sh
SwissProt_40:HV31_HUMAN	+	279.50	443.90	4.2e-17	119   P01770 homo sapiens (human)
SwissProt_40:HV3D_HUMAN	+	279.00	442.90	4.6e-17	122   P01769 homo sapiens (human)
SwissProt_40:HV43_MOUSE	+	277.50	441.03	6.3e-17	115   P01765 homo sapiens (human)
SwissProt_40:HV48_MOUSE	+	277.50	439.50	7.3e-17	138   P03980 mus musculus (mouse)
SwissProt_40:HV3A_HUMAN	+	277.00	439.75	7.0e-17	122   P01762 homo sapiens (human)
SwissProt_40:HV42_MOUSE	+	275.50	437.73	9.4e-17	117   P01812 mus musculus (mouse)
SwissProt_40:HV39_MOUSE	+	275.50	437.66	9.4e-17	118   P01809 mus musculus (mouse)
SwissProt_40:HV36_MOUSE	+	274.50	436.22	1.2e-16	116   P01806 mus musculus (mouse)
SwissProt_40:HV2D_HUMAN	+	274.50	435.60	2.9e-16	125   P01817 homo sapiens (human)
SwissProt_40:HV20_MOUSE	+	270.00	428.70	2.9e-16	122   P01789 mus musculus (mouse)
SwissProt_40:HV22_MOUSE	+	269.50	427.84	3.2e-16	123   P01791 mus musculus (mouse)

SwissProt\_40:HV50\_MOUSE + 268.00 425.68 4.3e-16 120 | P06329 mus musculus (mous  
SwissProt\_40:HV3K\_HUMAN + 268.00 425.27 4.3e-16 126 | P01772 homo sapiens (huma  
SwissProt\_40:HV16\_MOUSE + 268.00 424.63 4.3e-16 136 | P01783 mus musculus (mous  
SwissProt\_40:HV18\_MOUSE + 267.50 424.69 4.8e-16 123 | P01787 mus musculus (mous  
SwissProt\_40:HV04\_MOUSE + 266.50 423.53 5.8e-16 117 | P01748 mus musculus (mous  
seq\_name: SwissProt\_40:HV21\_HUMAN

seq\_documentation\_block:

ID HV21\_HUMAN STANDARD; PRT; 146 AA.  
AC P06331;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-II region ARH-77 precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85205332; PubMed=3922855;  
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;  
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-  
RT repeat sequence in 5' flanking region.";  
RL Gene 33:181-189(1985).  
DR PIR; A02101; GIHUH2.  
DR HSSP; P01825; 7FAB.  
DR InterPro; IPR003006; Iq\_MHC.  
DR InterPro; IPR003596; Iq\_v.  
DR Pfam; PF00047; ig; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION ARH-77.  
FT DOMAIN 20 117 V SEGMENT.  
FT DOMAIN 118 127 D SEGMENT.  
FT DOMAIN 128 146 J SEGMENT.  
FT DISULFID 42 115 BY SIMILARITY.  
FT NON\_TER 146 146  
SQ SEQUENCE 146 AA; 16228 MW; 8D7PD52BB218171F CRC64;

alignment\_scores:

Quality: 444.50 Length: 151  
Ratio: 3.735 Gaps: 7  
Percent Similarity: 78.808 Percent Identity: 66.887

alignment\_block:

US-09-019-441-2 x HV21\_HUMAN ..

Align seg 1/1 to: HV21\_HUMAN from: 1 to: 146

1 ATGAACACCTGTGTTCTTCTCTCTCTGTCGAGTCCAGATGG... 48  
1 MetLysHisLeuTrpPheLeuLeuLeu.TrpCysGlnLeuProaspValG 17  
49 ..GTCCTGTCCAGCTCAGCTCAGAGTGCGGCCAGGAGTGGTGAAG 96  
17 lYValLeuSerGlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuVallys 33  
97 CCTTCGGAGACCTGTCTCTACCTGCGTGTCTCTGCTGCTGTCTG 146  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
34 ProSerGluThrLeuSerLeuThrCysAlaValPheGlyGlySerPhe.. 49  
147 CAGTAGTAACCTGGGACCTGGATCCGCCAGCCCGGAGGAGGACTGG 196  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
50 .SerGlyTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrp 66  
197 AGTGGATTGACGATCTCTGTTAGTGGTGGGCGGCACCACTACAAAC 246  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
66 luTrpIleGlyIleAsnHisSer...GlySerThrAsnTrpLysThr 81





## alignment\_block:

US-09-019-441-2 x HV2G\_HUMAN

Align seg 1/1 to: HV2G\_HUMAN from: 1 to: 117

```
58 CAGCTGCAGTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTGGGAGAC 107
|||||
1 GlnValGlnLeuGlnSerGlyProGlyLeuValArgProSerGlnTh 17
108 CCTGTCCCTCACCTGCCTCTCTCTGTGTGGCTCTGTGCAGCAGTAGTAAC 157
|||||
17 rLeuSerLeuThrCysThrValSer...GlySerThrPheSerAsnAspT 33
158 GGTGGACCTGGATCCGCCAGCAGTCCAGGGAAGGACTGGAGTGGATTGGA 207
|||||
33 yTyThrTrpValArgGlnProProGlyArgGlyLeuGluTrpIleGly 49
208 CGTATCTCTGTGTAGTGTGGGGCCACCACTACAAACCCGTCCTCAAGAG 257
|||||
50 TyrValPheTyrlsGlyThrSerAspAspThrPro...LeuArgSe 65
258 TCAGATCATATTTCACAGACAGCTCCAGAACCCAGTCTCCCTGAACC 307
|||||
65 rArgValThrMetLeuValAspThrSerLysAsnGlnPheSerLeuArgL 82
308 TGAACCTCTGTACCGCGCGGACACGCGCTGTATTACTGTGCCAGAGAT 357
|||||
82 euSerSerValThrAlaAlaAspThrAlaValTyTyCysAlaArgAsn 98
358 TGGGCCCCAATAGCTGGAACACGCTAGGCTTCTGGGGCCAGGAGTCTCT 407
|||||
99 .....LeuIleAlaGly...CysIleAspValTrpGlyGlnGlySerLe 112
408 GGTCAACGCTCTCTCTCA 423
|||||
112 uValThrValSerSer 117
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seq\_name: SwissProt\_40:HV60\_MOUSE

## seq\_documentation\_block:

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ID HV60_MOUSE STANDARD; PRT; 116 AA.
AC P18531.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
DR PIR; J05059; HVMS31.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 18
FT CHAIN 19 116 - IG HEAVY CHAIN V REGION M315.
FT DOMAIN 19 48 FRAMEWORK-1.
FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 54 67 FRAMEWORK-2.
FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 40 114 BY SIMILARITY.
FT NON_TER 116
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SQ SEQUENCE 116 AA; 13095 MW; 4562E03E53DC9E10 CRC64;

## alignment\_scores:

Quality: 367.00 Length: 118  
Ratio: 3.634 Gaps: 2  
Percent Similarity: 85.593 Percent Identity: 62.712

## alignment\_block:

US-09-019-441-2 x HV60\_MOUSE

Align seg 1/1 to: HV60\_MOUSE from: 1 to: 116

```
1 ATGAACACACCTGTGGTCTTCCCTCCTGTGGCAGCTCCACAGATGGGT 50
|||||
1 MetLysValLeuSerLeuLeuThrAlaIlePro...GlyIi 16
51 CTRGTCCAGCTGCAGCTCAGGAGTCGGGCCAGGAGTGGTGAAGCCTT 100
|||||
16 eLeuSerAspValGlnLeuGlnGlySerGlyProGlyLeuValLysProS 33
101 CGGAGACCTGTCCCTCACCTGCCTGTCTCTGTGTGGCTCTGTGCAGCAGT 150
|||||
33 erGlnSerLeuSerLeuThrCysSerValThrGlyTySerIleThrSer 49
151 AGTAACCTGTGGACCTGGATCCGCCAGCAGTCCAGGGAAGGACTGGAGTG 200
|||||
50 GlyTyThrTrpAsnTrpIleArgGlnPheProGlyAsnLysLeuGluTr 66
201 GATTGGACGTATCTCTGTGTAGTGTGGGGCCACCACTACAAACCCGTCCT 250
|||||
66 pMetGlyTyIleSer...TyrAspGlySerAsnAsnTyrAsnProSerL 82
251 TCAAGAGTCGAGTCATCATTTCAACACACGCTCCAGAACCCAGTCTCTCC 300
|||||
82 euLysAsnArgIleSerIleThrArgAspThrSerLysAsnGlnPhePhe 98
301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCTGTATTACTGTGC 350
|||||
99 LeuLysLeuAsnSerValThrThrGluAspThrAlaThrTyTyTyCysAl 115
351 CAGA 354
|||||
115 aaArg 116
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seq\_name: SwissProt\_40:HV02\_XENLA

## seq\_documentation\_block:

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ID HV02_XENLA STANDARD; PRT; 135 AA.
AC P20957;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region XIgI4 precursor (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88176921; PubMed=2451244;
RA Schwager J., Mikoryak C.A., Steiner L.A.;
RT "Amino acid sequence of heavy chain from Xenopus laevis IgM deduced
from cDNA sequence: implications for evolution of immunoglobulin
domains.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:2245-2249(1988).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
```





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alignment_scores:
  Quality: 311.00
  Ratio: 3.274
  Percent Similarity: 81.197
  Length: 117
  Gaps: 2
  Percent Identity: 54.701

alignment_block:

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FT	DOMAIN	133	147	J SEGMENT.
FT	NON_TER	147	147	
SQ	SEQUENCE	147 AA;	16323 MW;	FCBCDB3D00FB6666 CRC64;

RT "The galactan-binding immunoglobulin Fab J539: an X-ray diffraction study at 2.6-A resolution.";  
RT Proteins 1:74-80(1986).  
RL -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN T  
CC RINDS GALACTAN  
CC

CC  
DR BLINDS GALACIAN.  
DR PIR; A02080; AVMSJ5.  
DR PDB; 2FBJ; 15-OCT-90.

DR InterPro; IPR003596; Iq\_v.  
DR InterPro; IPR003596; Iq\_v.  
DR InterPro; IPR003596; Iq\_v.

```
DR FLAM; FE000477; 19; 1.
DR SMART; SM00406; 1GV; 1.
```

KW Immunoglobulin V region; 3D-structure.

FT	NON_TTER	119	119
FT	STRAND	3	7

FT	STRAND	10	12
FT	STRAND	10	12

FT	14	15
TURN		
FT	18	25
STAND		

FT	STANDARD	19	29	31
FT	HELIX	29	29	31

FT	STRAND	34	39
FT	STRAND	41	46

FT	41	42
TURN	41	51
STRAND	45	

F'T	TURN
53	53
54	54

FT	STRAND	58	60
FT	TURN	62	67

FT	STRAND	68	72
1	1	1	1
2	2	2	2
3	3	3	3
4	4	4	4
5	5	5	5
6	6	6	6
7	7	7	7
8	8	8	8
9	9	9	9
10	10	10	10
11	11	11	11
12	12	12	12
13	13	13	13
14	14	14	14
15	15	15	15
16	16	16	16
17	17	17	17
18	18	18	18
19	19	19	19
20	20	20	20
21	21	21	21
22	22	22	22
23	23	23	23
24	24	24	24
25	25	25	25
26	26	26	26
27	27	27	27
28	28	28	28
29	29	29	29
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32	32	32	32
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47	47	47	47
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52	52	52	52
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73	73	73	73
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90	90	90	90
91	91	91	91
92	92	92	92
93	93	93	93
94	94	94	94
95	95	95	95
96	96	96	96
97	97	97	97
98	98	98	98
99	99	99	99
100	100	100	100

FT	STRAND	78	83
FT	HEI IY	88	90

FT	HELIX	92	100
FT	STRAND	92	100

FT	TURN	101	103
CE	CE	104	108

FT	STRAND	104	108
ET	STRAND	112	116

SQ SEQUENCE 119 AA; 13240 MW; 577B4F1DB675C1F1 CRC64;

alignment\_scores:

Quality:	303.00	Length:	122
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Ratio:	3.061	/	Gaps:	3
Percent Similarity:	81.748		Percent Identity:	50.000

SECRET

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alignment_block:
  115 00 010 441 2  " 11540 MONCE
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```
US-09-019-441-Z X HV40_MOUSE ..
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Align seg 1/1 to: HV40\_MOUSE from: 1 to: 119

58 CAGCTGCAGCTGCAGGAGTGGGGCCAGGAGTGGTGAAGCCTTCGGAGAC 107

[illegible]

1 GluValLysLeuLeuGluSerGlyGlyGlyLeuValGlnProGlyGly 17

108 CCTGTCCCTCACCTGCCGTGTCTCTGGTGGCTCTGTCTCAGCAGTAGTAAC 157

[illegible]

17 rLeuLysLeuSerCysAlaAlaSerGlyPheAspphe...SerLysTyrT 33

158 GTGGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTGGATTGGA 207

[illegible]

33 rpMetserTrpValArgGlnAlaProGlyLysGlyLeuGluTrpIleGly 49

208 CGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCCTCAAGAG 257

5  
5  
C  
D  
T  
E  
F  
H  
I  
J  
K  
L  
M  
N  
O  
P  
Q  
R  
S  
T  
U  
V  
W  
X  
Y  
Z

30 GIUTEHSPIOASPSERGTYIMILEASNTYIMIPROSEILEULYSAS 00

258 TCGAGTCATCATTTCAACAAGACACGTCCTCAAGAACAGTTCTCCCTGAACC 307

[illegible]

```

66 pLysPheIleIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuGlnM 83
308 TGAACCTCTGTGACCGCGCGGACACGGCCGCTATTACTGTGCCAGAGAT 357
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 etSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArg... 98
358 TGGGCCCAATAGCTGGACACACCTAGGCTTCTGGGGCCACGGAGTCCT 407
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99 ...LeuHisTyrTyrGlyTyrAsn...AlaTyrTrpGlyGlnGlyThrLe 113
408 GGTCAACGCTCTCCCTCA 423
113 uValThrValSerAla 118

seq_name: SwissProt_40:HV37_MOUSE

seq_documentation_block:
ID HV37_MOUSE STANDARD; PRT; 119 AA.
AC P01807;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region X44.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=79223895; PubMed=111245;
RA Rao D.N., Rudikoff S., Kruttsch H., Potter M.;
RT "Structural evidence for independent joining region gene in
RT immunoglobulin heavy chains from anti-galactan myeloma proteins and
RT its potential role in generating diversity in
RT complementarity-determining regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979).
CC 1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS GALACTAN.
DR PIR; A02077; AVMSX4.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13246 MW; BC34FC8F31CD41B3 CRC64;

alignment_scores:
Quality: 298.00 Length: 126
Ratio: 3.072 Gaps: 3
Percent similarity: 76.984 Percent Identity: 47.619

alignment_block:
US-09-019-441-2 x HV37_MOUSE

Align seg 1/1 to: HV37_MOUSE from: 1 to: 119

58 CAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGGTGAAGCTTCGGAGAC 107
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1 GluValLysLeuLeuGluSerGlyGlyLeuValGlnProGlyGlySe 17
108 CTGTCTCCTCACCTGCCTCTCTCTGTGGTCTGTGTGCTGTGTGCTAGTAACT 157
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17 rLeuLysLeuSerCysAlaAlaSerGlyPheAspPhe...SerArgTyrT 33
158 GGTGGACCTGGATCCGCCACCCAGGAGGAGTGGAGTGGATTGGA 207
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
33 rpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpIleGly 49
208 CGTATCTGTGTGTGGGGCCACCACTACAACCCGTCCTCAAGAG 257
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

50 GluIleAsnProAspSerSerThrIleAsnTyrThrProSerLeuLysAs 66
258 TCGAGTCTCATCTTTCAACAAGACACGTCCTCAAGAACCACTTCTCCCTGAACC 307
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
66 pLysPheIleIleSerArgAspAsnAlaLysAsnThrLeuTyrLeuGlnM 83
308 TGAACCTCTGTGACCGCGCGGACACGGCCGCTATTACTGTGCCAGA... 354
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 etSerLysValArgSerGluAspThrAlaLeuTyrTyrCysAlaArgLeu 99
355 .....GATTGGGCCCAATAGCTGGACACACGCTAGGCTTCTGGGG 395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
100 HisTyrTyrGlyTyrAla.....AlaTyrTrpGly 109
396 CCAGGGAGTCTGTGTGCTCACCGTCTCTCTCA 423
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
109 yGlnGlyThrLeuValThrValSerAla 118

```





99 LeuLysLeuSerSerValAsnAlaAlaAspThrAlaValTyrTyrCysAl 115

351 CAGAGATTGGGCCCCAAATAGCTGGAACAACGCTAGGC..... 387

115 aArgValIleThrArgAlaSerProGlyThrAspGlyArgTyrGlyMetA 132

368 :...TCGGGCGCCAGGGAGGCTCGCGTCACCCGCTCTCCCTC 423  
 |||||  
 132 spValTrpGlyGlnClyThrThrValThrValSerSer 144  
 |||||  
 Name: sp human:Q96AA6

documentation\_block:  
Q96AA6 PRELIMINARY; PRT; 618 AA.  
Q96AA6;

01-DEC-2001	(TrEMBLrel. 19, Created)
01-DEC-2001	(TrEMBLrel. 19, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
HYPOTHETICAL 67.8 KDA PROTEIN.

Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele-

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo;  
NCBI\_TaxID=9606;

[1] SEQUENCE FROM N.A. TESTED UNDER THE CONDITIONS

Strausberg R.;  
submitted (NOV-2001) to the EMBL/Genbank/NCBI databases  
TISSUE=LYMPH, AND LYMPHOMA;

EMBL; BC017356; AAH17356.1; -.  
Submitted (NOV-2001) to the EMBL/Genbank/DDBJ databases.  
hypothetical protein

hypocretin-like protein.  
SEQUENCE 618 AA; 67758 MW; 96DBD4C7C696E0A6 CRC64;

ment scores:

Quality:	499.50	Length:	146
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alignment_block:
US-09-019-441-2 x Q96AA6 ..
percent similarity: 84.24 percent identity: 70.54

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ATTN: SEC 1/1 CO: 220000

1 MetLysHisLeuTrppPheLeuLeuValAla

51 CCTGTCCCGAGCTGCAGCTGCAGGAGTCGGGGCCAGGAGTGGTGAAGCCTT 100  
|||||:::|||||::: ||| |||:::|||||  
17 lLeuSerGlnValGlnLeuGlnGlnTrpGlyAlaGlyLeuLeuLysProS 34

101 CGGAGACCTGTCCTCCCTCACCTGGGTGTCTCTGGTGGCTGTGTGACGAGT 150  
34 erGluThrLeuSerLeuThrCysGlyValTyrglyGlySerPhe...Ser 49			

201 GATTGGACGATCTCTGCTAGTGGTGGGGGCCACCAACTACAACCCCGTCCC 250  
 |||:::||||::: ||| |||:::|||||:::|||||  
 66 pIleGlyGluIleAsnHisSer...GlySerThrAsnTyrAsnProSerL 82

251 TCAAGAGTCGAGTCATCATTTTCACAAGACACACGTCCAAAGAACCAGTTCCTCC 3000  
 |||  
 82 euLysSerArgValThrIleSerValAspThrSerLysLysGlnLeuSer 98

301 CTGAACCTGAACTCTGTGACCGCCGGGCACGCCGTATTACTGTGC 350  
|||||::|||::|||::|||::|||::|||::|||::|||  
99 LeuLysLeuSerSerValAsnAlaAlaAspThrAlaValTyrCysAl 115

351 CAGAGATTGGGCCCCAAATAGCTGGAACAACGCTAGGC..... 387





101	CGGAGACCTGTCCCTCACCTGCCTTCGGTGTCTCTGGTGCGCTCTGTCTCAGCAGT	150
11	:     :     :     :     :     :     :     :     :	
34	erGlnSerLeuSerIleThrCysThrValSerGlyPheAlaLeuThrSer	50
151	AGTAACCTGGTGGACTCGATCCGCCACGCCCCCAGGGAAGGCACTGGAGTG	200
51	TyrAla...lleSerTrpValArgGlnProProGlyLysGlyLeuGluTr	66
201	GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCACAACATAACAACCGTCCC	250
66	pLeuGly...ValIleTrpThrGlyGlyValThrAsnTyrAsnSerAlaL	82
251	TCAAGAGTCGAGTCATCATTTACAAGACACAGCTCCAAGAACAGCTTC	300
82	eulySerArgLeuSerIleSerLyaspAsnSerLysserGlnvalPhe	98
301	CTGAACCTGAACCTCTGTGACCGCGCGGACACAGCCGCTGTATTACTGTGC	350
99	LeuLysMetAsnSerLeuGlnThrAsnAspThrAlaArgTyrTyrcysAl	115
351	CACAGATTTGGCCCCAATACTGGAAACAACGCTAGGCTTCTGGGGCCAGG	400
115	aArgASP...SerAsnTyrGluGly...AlaMetAspTyrTrpGlyGlnG	130
401	GAGTCCTGTGTCACCGTCTCCTCA	423
130	lyThrSerValThrValSerSer	137
seq_name: sp_rodent:Q99NG4		
seq_documentation_block:		
ID	Q99NG4	PRT; 121 AA.
AC	PREIMINARY;	
DC	Q99NG4;	
DT	01-JUN-2001 (TREMBLrel. 17, Created)	
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)	
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE	SINGLE CHAIN FV (FRAGMENT).	
OS	Mus musculus (Mouse).	
OQ	Plasmid PHEN1.	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo	
OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae	
NCBI_TaxID=10090;	[1]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN-BALB/C;	
RX	MEDLINE=98169018; PubMed=9510199;	
RA	Hawiltsch H., Frank R., Hennecke M., Baensch M., Sohns B., A	
RT	Bautsch W., Kola A., Klos A., Koehl J.;	
RL	"Site-Directed C3a-Receptor Antibodies from Phage Display L	
DR	J. Immunol 160:2947-2958(1998).	
DR	EMBL; AJ222590; CAA10890.1; -	
DR	HSSP; P01825; 7FAB.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR003600; Ig_like.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	InterPro; IPR003596; Ig_v.	
DR	Fram; PF00047; Ig; 1.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00406; IGV; 1.	
DR	SMART; SM00410; IG_like; 1.	
KW	Plasmid.	
FT	NON_TER	1
FT	NON_TER	121
SQ	SEQUENCE	121 AA; 13255 MW; D293B4EBC8C59D5B CRC64;

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alignment_scores:
  Quality: 336.00
  Ratio: 3.360
  Percent Similarity: 81.967

alignment_block:
  US-09-019-441-2 x Q99NG4
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Align seg 1/1 to: Q99NG4 from: 1 to: 121

[illegible]

seq\_name: sp\_human:096BB9

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seq_documentation_block:
ID Q96BB9 PRELIMINARY; PRT; 597 AA.
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seq_documentation_block:
ID   Q96BB9          PRELIMINARY;      PRT;      597 AA.
AC   Q96BB9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   HYPONETICAL 65.0 KDA PROTEIN.
OS   Homo sapiens (Human)..
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA   Strausberg R.;
RL   Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR   EMBL; BC015760; AAH15760.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

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alignment_scores:		
Quality:	328.50	Length: 141
Ratio:	3.221	Gaps: 3
Percent Similarity:	72.340	Percent Identity: 51.064

alignment block:

US-09-019-441-2 x Q96BB9

Align seg 1/1 to: Q96BB9 from: 1 to: 597

13 TGGTCTCTCCTCCTCGTGTCGAGCTCCACAGATGGGTCTCGTCCAGCT 62  
|||||  
7 TrpLeuphe.....LeuValAlaIleLeuLysGlyValGlnCysGluVa 21  
63 GCAGCTGCAGAGATGCGGCCCGCCAGAGATGGTGAAGCCTTCGGAGACCCTGT 112

:||||| ||||||| |||:||||:||||: :|||  
 21 lGlnLeuLeuGluSerGlyGlyLeuValGlnProGlyGlySerLeu 38  
 113 CCCTCACCTCGCTCTCTGGTGGCTTCGACGACGAGTAGTAACGTGGTG 162  
 :|||:||||| ||||||| |||:|||||  
 38 rGluSerCysAlaAlaSerGlyPheSerPheSerSerTyrAla...Met 53  
 163 ACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTGGATTGGACGAT 212  
 :|||:||||| ||||||| |||:|||||  
 54 AsnTnpValArgGlnAlaProGlyLysGlyLeuGlnTrpValSerAlaI 70  
 213 CTCTGGTAGTGTGGGGCCACCAACTACACCCGTCCTCTCAAGAGTCGAG 262  
 |||||:||||| |||:|||||  
 70 eSerGlySerGlyGlySerThrTyrTyrAlaAspSerValLysGlyArg 87  
 263 TCATCATTTTCAAGACACGTCCTCAAGAACCACTCTCCCTCAACCTGAAC 312  
 87 heThrIleSerArgAspAsnSerArgAspThrLeuTyrLeuGlnMetAsn 103  
 313 TCTGTGACCCCGCGGACAGCGCGCTGATTACTGTGTCAGAGATTGGCC 362  
 |||:||||| ||||||| |||:|||||  
 104 SerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysAspProAr 120  
 363 CCAAAATAGCTGGA.....ACAACGCTAGGCTCTCTGGGCCAGG 400  
 :|||:|||||  
 120 gGlyTyrSerAlaSerGlyAsnTyrThrArgGluAspTyrTrpGlyGlnG 137  
 401 GAGTCCTGGTCCACCGTCTCTCTCA 423  
 137 lyThrLeuValThrValSerSer 144

seq\_name: sp\_rodent:Q9QYF0

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seq_documentation_block:
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
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AC	QOQYFO;	
AD	01-MAY-2000 (TrEMBLrel. 13, Created)	
AE	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
AF	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
AG	CN 8 SCFV.	
AH	CN 8.	
AI	GN	
AJ	Mus musculus (Mouse).	
AK	OS	
AL	OC	
AM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	
AN	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus	
AO	OX	
AP	[1]	
AQ	SEQUENCE FROM N.A.	
AR	RP	
AS	RC	
AT	STRAIN=BALB/C; TISSUE=SPLEEN;	
AV	RX	
AW	MEDLINE-20183931; PubMed-10705631;	
AX	RA	
AY	Shinohara N., Demura T., Fukuda H.;	
AZ	RT	
BA	'Isolation of a vascular cell wall-specific monoclonal antibody	
BB	recognizing a cell polarity by using a phage display subtraction	
BC	method.';	
BD	Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).	
BE	RE	
BF	EMBL; AB036341; BAA88633.1; ..	
BG	DR	
BH	HSSP; P01607; 1REI	
BI	DR	
BJ	InterPro; IPR003006; Ig_MHC.	
BK	DR	
BL	InterPro; IPR003596; Ig_v.	
BM	DR	
BN	Pfam; PF00047; Ig_2.	
BO	DR	
BP	SMART; SM00406; IGV; 2.	
BQ	DR	
BR	SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;	

alignment scores:

Quality:	324.50	Length:	144
Ratio:	2.897	Gaps:	4
Percent Similarity:	77.778	Percent Identity:	48.611

alignment block:

US-09-019-441-2 x Q9QYF0

Align seq 1/1 to: Q9QYF0 from: 1 to: 298

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alignment_block:
US-09-019-441-2 x Q9UL74  ..
Align seg 1/1 to: Q9UL74 from: 1 to: 118

85  GGAGTGGTGAAGCCTTCGGAGACCCCTGCCTCACCTCGCTGCTCTCGG 134
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1  GlyLeuValLysProSerGlnThrLeuSerLeuThrCysAlaIleSerG1 17
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

135  TGGCTCTGTCAGCAGT...AGTAACTGGTGACCTGGATCGCCAGCCGC 181
    - |||||:|||||:|||||:|||||:|||||:|||||:|||||
17  yaspSerValSerSerAsnSerAlaAlaTrpAsnCysIleargProValp 34
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

182  CAGGGAAGGAGCTGGAGTGGATTGAGCTATCTCT...GGTAGTGGTGGG 228
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  roSerArgGlyLeuGluTrpLeuclYargThrThrTyArgSerLysTrp 50
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

229  GCCACCAACTACAAACCCGTCCTCCCTCAAGAGTCGAGTCATCTTCAACA 278
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51  TyrAsnAspTyrAlaValSerValLysSerArgIleThrIleAsnProAs 67
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279  CAGTCCCAAGAACCCAGTTCCTCCCTGAACCTGAACCTCTGTGACCGCGGG 328
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67  pThrSerLysAsnGlnPheSerLeuGlnLeuAsnSerValThrProGluA 84
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329  ACAGCGCCGTGTATTACTGTGCCAGA.....GATTGGGCCCAATA 369
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84  spThrAlaValTyrTyrcysAlaSerThrThrLeuAsnTrpGlyTyrGlu 100
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370  GCTGGAAACAACGCTAGCGTTCCTGGGGCCAGGAGTCCTGGTCACCGCTCTC 419
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420  CTC A 423
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ID Q9UL88 PRELIMINARY;
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AE	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
AF	01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
AG	MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION	
AH	(FRAGMENT).	
AI		
AJ	OS Homo sapiens (Human).	
AK	OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AL	OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
AM	OX NCBI_TaxID=9606;	
AN	[1]	
AO	SEQUENCE FROM N.A.	
AP	RP MEDLINE=98277139; PubMed=9614934;	
AQ	RX Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,	
AR	RA Young D.C.;	
AS	RT "Myosin-reactive autoantibodies in rheumatic carditis and normal	
AT	RT fetus.";	
AV	RL Clin. Immunol. Immunopathol. 87:184-192(1998).	
AW	DR ENBL; AF035026; RAD56262.1; -.	
AX	DR HSSP; P01810; 2FBU.	
AY	DR InterPro; IPR003006; Ig_MHC.	
AZ	DR InterPro; IPR003596; Ig_V.	
BA	DR Pfam; PF00047; Ig; 1.	
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BL	FT NON_TER 131	
BM	FT NON_TER 131	
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Date: Sep 23, 2002 10:06 AM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
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-Q/cgn2\_1/USPTO\_spool/US09019441/runat\_23092002\_095257\_6281/app\_query.fasta\_1.1860  
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-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
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## Search information block:

Query: US-09-019-441-2  
Query length: 423  
Database: A\_Geneseq\_032802.\*  
Database sequences: 747574  
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AC AAB36206;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Human immune system associated protein HISAP-4.  
XX  
KW Human; immune system associated protein; HISAP-4; immune disorder;  
KW infection; autoimmune disease; cancer.  
XX  
OS Homo sapiens.  
XX  
PN US6135941-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 27-MAR-1998; 98US-0049672.  
XX  
PR 27-MAR-1998; 98US-0049672.  
XX  
PA (INCY- ) INCYTE PHARM INC.  
XX

Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;  
Hillman JL, Au-Young J;  
WPI: 2001-030926/04.  
DR N-PSDB; AAC66522.

XX  
PT New human immune system associated proteins (HISAP) and polynucleotides  
encoding the HISAP, useful for diagnosing, treating or preventing  
immune or cell proliferative disorders or infections  
XX  
PS Claim 1; Column 53-56; 54pp; English.

XX  
CC The present invention provides the coding and protein sequences for a  
number of human immune system associated proteins (HISAPs). These can be  
used in the diagnosis and treatment of various autoimmune disorders,  
infections and cell proliferation diseases. The diseases include AIDS,  
adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,  
Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia  
gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus  
erythematosus, arteriosclerosis, cirrhosis and cancer.

SQ Sequence 473 AA;

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Ratio: 4.333 Gaps: 3  
Percent Similarity: 89.583 Percent Identity: 78.472

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US-09-019-441-2 x AAB36206

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1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17

51 CCTGTCCACAGTCGACGTGCAGGAGTCGGCCCGAGAGTGTGTGAAGCCTT 100

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17 lLeuSerGlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysProS 34

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CC  antibody.
XX
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51  CCTGTCCCCAGCTCAGCTGCAGAGTCGGGCCCAGGAGTGGTGAAGCCTT  100
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17  lleuSerGlnValGlnLeuGlnGluSerGlyProGlyValValLysProS  34

101 CGGAGACCCTGTCCCTACACTGCCTCTCTCTGTGTGCTCTCTGCACGAGT  150
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34  erGluThrLeuSerLeuThrCysGThrValSerGlyGlySerPhe...Ser  49

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 50 ThrTyrTyrTrpAsnTrpIleArgGlnProProGlyLysGlyLeuGluTr 66  
 201 GATTGGACGTACTCTCGTGTAGTGGTGGGCCACCACTACAACCCGTCCTC 250  
 66 pIleGlyTyrIleGlyGlyGlyGlyArgProAsnTyrAsnSerLeu 83  
 251 TCAAGAGTCGAGTCATCATTTTCACAAGACAGCTCCAAAGAACCACTGTCCTC 300  
 83 euLysSerArgIleThrLeuSerLeuAspAlaSerLysAsnGlnPheSer 99  
 301 CTGAACCTGNACTCTGTGACCGCCGCGGACACGCGCGTGTATTACTGTCTGC 350  
 100 LeuAsnLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 116  
 351 CAGAGATTGGGCCCAAAATAGCTGGGAACA...ACGCTAGGCTTCTGGGGCC 397  
 116 aArgAspArgGlyTyrGlyAlaSerAsnAspAlaPheAspThrP6GlyG 133  
 398 AGGAGTCTCGTCAACCGCTCTCTCTCA 423  
 133 InGlyLeuArgValThrValSerSer 141

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116 aArgAspArgGlyTyrGlyAlaSerAsnAspAlaPheAspThrGlyG 133  
398 AGGGAGTCCTGGTCACCGTCTCCTCA 423  
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XX DT 18-OCT-1997 (first entry)
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XX Human gamma-4pE heavy chain.
XX
XX CD4; monoclonal antibody; chimaeric antibody; recombinant antibody
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;

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KW	leukaemia; lymphoma; graft-versus-host disease; asthma;
KW	transplant rejection; HIV; therapy; CS9 gamma 4PE.
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XX	Homo sapiens.
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FH	Key
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FT /note= "site of L236E mutation"

XX	WO9709351-A1.
XX	13-MAR-1997.
XX	05-SEP-1996; 96WO-US14324.
XX	06-SEP-1995; 95US-0523894.
XX	(IDEC-) IDEC PHARM CORP.
XX	Hanna N, Newman RA, Reff ME;
PI	WPI: 1997-201913/18.
DR	N-PSDB; AAT62870.
XX	Chimeric antibody comprising monkey variable domains and hu-
PT	constant domains - affects CD4-mediated immune functions,
PT	useful for treatment of autoimmune disease, e.g. rheumatoid
PT	arthritis
XX	Claim 6: Page 91-93; 155pp; English.
XX	3 Polypeptides (AAW14925-27) respectively comprise the heav-
CC	regions of human gamma-4, gamma-4E carrying an L236E mutat-
CC	the hinge region, and gamma-4PE carrying L236E and S229P mu-
CC	They can be incorporated into novel monoclonal and chimeric
CC	antibodies, e.g. CE9 gamma-4, CE9 gamma-4E and CE9 gamma-4
CC	which the human IgG4 Fc binding domain framework is combin-
CC	the antigen binding domains (see also AAW14922-23) of macac-
CC	human CD4 monoclonal antibody E9.1. These antibodies show
CC	affinity to human CD4, have little or no immunogenicity in
CC	and show reduced or absence of effector function. The gam-
CC	-4PE mutations confer activity enhanced stability and elimi-
CC	depleting activity. The antibodies can be used to treat a
CC	diseases such as rheumatoid arthritis.
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51 CCTGTCCCAGCTGCAGTCGAGGAGTGGGCCAGGAGTGGTCAGGCTT 100	
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101 CGGAGACCCTGTCCCTCACCTCGGCTGTCTCTGTGGTGGCTCTGTCCAGCAGT 150	
34 erGluThrLeuSerLeuThrCysSerValSerGlySerIleSerGly 50	
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351 CAGAGAT.....TGGGCCCAATAGCTGGAACAACGC 382
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117 aserAsnIleLeuLysTyrLeuHisIrp.....L 127
383 TAGGCTTCTGGGCGCAGGAGTCTGGTCACCTCTCTCA 423
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127 euLeuTyrTrpGlnGlyValLeuValThrValSerSer 140

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alignment scores:

Quality: 555.50

Length: 147

Ratio: 4.480

Gaps: 2

Percent Similarity: 84.354

Percent Identity: 74.830



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11 .....
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT:AAW32477
seq_documentation_block:
ID AAW32477 standard; Protein; 140 AA.
XX
AC AAW32477;
XX
DT 16-JAN-1998 (first entry)
XX
DE Anti-CD4 cynomolgus monkey immunoglobulin heavy chain variable region.
XX
KW Anti-CD4 antibody; cynomolgus monkey; immunoglobulin; Ig;
KW chimpanzee; chimeric antibody; human therapy; Old World monkey;
KW antigen binding region; tumour.
XX
OS Macaca fascicularis.
XX
PN US5658570-A.
XX
PD 19-AUG-1997.
XX
PF 25-JUL-1991; 91US-0735064.
XX
PR 10-JUL-1992; 92US-0912292.
PR 25-JUL-1991; 91US-0735064.
PR 23-MAR-1992; 92US-0856281.
PR 25-JAN-1995; 95US-0379072.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Hanna N, Newman RA, Raab RW;
XX
DR WPI; 1997-424183/39.
DR N-PSDB; AAT91564.
XX
PT Chimeric antibodies for human therapy - comprising human or
PT chimpanzee immunoglobulin constant region and an Old World monkey
PT antigen-binding region
XX
PS Example 3; Fig 13; 46pp; English.
XX
CC A new chimeric antibody (Ab) has been developed comprising a human or
CC chimpanzee immunoglobulin (Ig) constant region and an Old World monkey
CC antigen (Ag)-binding region. The present sequence represents an anti-CD4
CC cynomolgus monkey Ig heavy chain variable region. An anti-CD4 antibody
CC (Ab) comprising the light- and heavy-chain variable regions encoded by
CC DNA corresponding to the present sequence, and that of AAT91565, is also
CC new. The Abs are useful for human therapy, especially of tumours. Old
CC world monkeys are sufficiently different from humans to allow Abs
CC against human Ags, even relatively conserved Ags such as CD4 and CD54,
CC to be raised in these monkeys, and are sufficiently similar to humans to
CC avoid host anti-Ab immune responses when the Abs are introduced into
CC humans.
XX
SQ Sequence 140 AA;
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alignment_scores:
Quality: 552.50      Length: 147
Ratio: 4.456        Gaps: 2
Percent Similarity: 84.354    Percent Identity: 74.150
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US-09-019-441-2 x AAW32477 ..
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1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
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51 CCTGTCCACGCTGCAGCTGCAGAGTCCGGCCAGAGTGGTGAAGCCTT 100
17 lLeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysPro 34
101 CGGAGACCCCTGCTCCCTCACCTGGCTGCTCTCTGCTGCTGTCAGCAGT 150
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50
151 AGTAACCTGGTGACCTGGATCCGCCAGCCGCCAGGAGGAGGAGTGGAGT 200
51 AspTyTrpTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67
201 GATTGGACGATCTCTCTGCTAGTGGTGGGGCCACCACTACAACCCGTCC 250
67 pIleGlyTyIleTyrglySerGlyGlyGlyThrAsnTyAsnProSerL 84
251 TCAAGAGTCGAGTCATCTTTCACAGACACGTCACAGAACACCACTTCTCC 300
84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGCTGTATTACTG 350
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyTrCysAl 117
351 CAGAGAT.....TGGGCCCAATAGCTGGAACAACGC 382
117 aSerAsnIleLeuLysTyTrLeuHisTrp.....L 127
383 TAGGCTTCTGGGCGCAGGAGTCTCTGTCACCGTCTCTCTCA 423
127 euleuTyTrpGlyGlnGlyValLeuValThrValSerSer 140
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seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT:AAW43430
seq_documentation_block:
ID AAW43430 standard; Protein; 140 AA.
XX
AC AAW43430;
XX
DT 05-MAY-1998 (first entry)
XX
DE Monkey anti-CD4 heavy chain variable region protein sequence.
XX
KW Primer; PCR; amplification; leader sequence; human; monkey; baboon;
KW macaque; immunoglobulin; heavy chain variable region; chimpanzee; hybrid;
KW lymphoma; AIDS; autoimmune disease; inflammatory disease; transplant;
XX tumour; antibody.
XX
OS Macaca cynomolgus.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "signal peptide"
FT Protein 20..140
FT /note= "mature protein"
XX
PN US5693780-A.
XX
PD 02-DEC-1997.
XX
PF 07-JUN-1995; 95US-0481869.
XX
PR 10-JUL-1992; 92US-0912292.
PR 25-JUL-1991; 91US-0735064.
PR 23-MAR-1992; 92US-0856281.
PR 25-JAN-1995; 95US-0379072.
PR 07-JUN-1995; 95US-0481869.
XX
PA (IDEC-) IDEC PHARM CORP.
XX
PI Hanna N, Newman RA, Raab RW;
XX
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XX 10-JUL-1992; 92US-0912292.  
PR 25-JUL-1991; 91US-0735064.  
PR 23-MAR-1992; 92US-0856281.  
PR 25-JAN-1995; 95US-0379072.  
PR 07-JUN-1995; 95US-0478039.  
XX (IDEC-) IDEC PHARM CORP.  
XX Hanna N, Newman RA, Raab RW;  
XX WPI; 1997-535052/49.  
DR N-PSDB; AAT95167.  
XX  
PT Production of humanised antibodies containing monkey variable region  
PT - used for the treatment of B cell lymphoma, autoimmune disease,  
PT inflammatory disease and infection, e.g. by HIV  
XX  
XX Example 3; Columns 107-108; 84pp; English.  
XX  
CC The present sequence is a monkey anti-human CD4 antibody  
CC heavy chain variable region, which was used in the development of  
CC a novel method for producing a chimeric antibody (Ab), comprising  
CC the variable region of an old world monkey (OWM) Ab and the  
CC constant region of a human Ab. The method comprises amplifying DNA  
CC from the OWM using a primer complementary to the 5' leader sequence  
CC of the OWM Ab gene and fusing the resulting variable region coding  
CC sequence with a human constant region coding sequence.  
CC The chimeric Ab may be used as a passive or active therapeutic for  
CC B cell lymphoma, infectious, e.g. AIDS, autoimmune and inflammatory  
CC diseases and transplant rejection. The Ab can be used in its native  
CC form or as part of an Ab/chelate, Ab/drug or Ab/toxin complex.  
CC Additionally, a whole Ab, or a fragment (Fab2, Fab, Fv) may be used  
CC as an imaging reagent or as a potential vaccine or immunogen in  
CC active immunotherapy to generate anti-idiotypic responses.  
CC An anti-CD4 recombinant Ab, or a fragment can also be used to  
CC induce immunosuppression and can therefore be used to treat or  
CC prevent resistance to, or rejection of transplanted organs or  
CC tissues, autoimmune, inflammatory, proliferative and  
CC hyperproliferative diseases, cutaneous manifestations of  
CC immunologically mediated diseases (e.g. rheumatoid arthritis, lupus  
CC erythematosus, systemic lupus erythematosus, Hashimoto's  
CC thyroiditis, multiple sclerosis, myasthenia gravis, type 1  
CC diabetes, uveitis, nephrotic syndrome, psoriasis, atopic  
CC dermatitis, contact dermatitis and further eczematous dermatitides,  
CC seborrheic dermatitis, lichen planus, Pemphigus, bullous pemphigus,  
CC Epidermolysis bullosa, urticaria, angioedemas, vasculitides,  
CC erythema, cutaneous eosinophilias, alopecia areata), reversible  
CC obstructive airways disease, intestinal inflammations and  
CC allergies (e.g. Coeliac disease, proctitis, eosinophilia  
CC gastroenteritis, mastocytosis, Crohn's disease and ulcerative  
CC colitis) and food related allergies (e.g. migraine, rhinitis and  
CC eczema).  
CC The Ab of the invention is non-immunogenic and therefore does not  
CC induce a human anti-Ab response. It also has a relatively long  
CC half-life and a full effector function with human cells and  
CC complement.  
XX  
SQ Sequence 139 AA;

alignment\_scores:  
Quality: 548.50 Length: 146  
Ratio: 4.459 Gaps: 2  
Percent Similarity: 84.247 Percent Identity: 73.973

alignment\_block:  
US-09-019-441-2 x AAW35284 ..

Align seg 1/1 to: AAW35284 from: 1 to: 139

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1 MetLysHisLeuTrpPheLeuLeuLeuValAlaAlaProArgTrpVa 17  
51 CCTGTCCAGCTGCAGCTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100  
|||||  
17 LeuSerGlnValGlnLeuGlnGluAlaGlyProGlyLeuValLysProS 34  
101 CGGAGACCTGTCCCTCACCTGGCTGCTCTGGTGGCTCTGTCAGCAGT 150  
|||||  
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50  
151 AGTAACCTGGTGGACCTGCATCCGCCAGCCAGGGAAGGAGTGGAGTG 200  
|||  
51 AspTyrTrpTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67  
201 GATGGACGATATCTCTGTAGTGGTGGGCCACCACTACAACCCGTCCTC 250  
|||||  
67 pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL 84  
251 TCAAGAGTCGAGTCATCATTTTCACAGACACGCTCCAGAACCACTTCTCC 300  
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84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100  
301 CTGAACCTGAACCTCTGTGACCGCGGCACACGCGCGCTGTATTACTGTGC 350  
|||||  
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117  
351 CAGAGAT.....TGGGCCCAATAGCTGGAACAACGC 382  
|||  
117 aserAsnIleLeuLysTyrLeuHisTrp.....L 127  
383 TAGGCTCTCGGCCAGGAGTCTGTGTCACCTCTCC 420  
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127 euleuTyrTrpGlyGlnGlyValLeuValThrValSer 139  
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seq\_documentation\_block:  
ID AAW14922 standard; Protein; 139 AA.  
XX  
AC AAW14922;  
XX  
DT 18-OCT-1997 (first entry)  
XX  
DE Monkey anti-CD4 heavy chain variable domain.  
XX  
KW CD4; monoclonal antibody; chimaeric antibody; recombinant antibody;  
KW cynomolgus monkey; autoimmune disease; rheumatoid arthritis;  
KW leukaemia; lymphoma; graft-versus-host disease; asthma;  
KW transplant rejection; HIV; therapy; CE9.1.  
XX  
OS Macaca cynomolgus.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= sig\_peptide  
FT /label= Mat\_protein  
XX  
PN WO9709351-A1.  
XX  
PD 13-MAR-1997.  
XX  
PF 05-SEP-1996; 96WO-US14324.  
XX  
PR 06-SEP-1995; 95US-0523894.  
XX  
PA (IDEC-) IDEC PHARM CORP.  
XX  
PI Hanna N, Newman RA, Reff ME;  
XX  
DR WPI; 1997-201913/18.  
DR N-PSDB; AAT62865.  
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/cgn2_6/ptodata/2/paa/US096_COMB	pep:US-09-612-914-10	+ 555.50	897.54	5.2e-42	467
/cgn2_6/ptodata/2/paa/US096_COMB	pep:US-09-612-914-12	+ 555.50	897.54	5.2e-42	467
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/cgn2_6/ptodata/2/paa/US096_COMB	pep:US-09-612-914A-10	+ 555.50	897.54	5.2e-42	467
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/cgn2_6/ptodata/2/paa/US095_COMB	pep:US-09-576-424-4	+ 524.50	846.50	3.5e-39	476
/cgn2_6/ptodata/2/paa/US060_COMB	pep:US-60-195-053-2233	+ 524.00	858.04	3.0e-39	126
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/cgn2_6/ptodata/2/paa/US097_COMB	pep:US-09-760-479-637	+ 521.00	840.67	7.4e-39	480
/cgn2_6/ptodata/2/paa/US091_COMB	pep:US-09-107-223A-2	+ 520.50	840.05	8.2e-39	470
/cgn2_6/ptodata/2/paa/US080_COMB	pep:US-08-004-730B-2	+ 519.50	849.54	8.0e-39	142
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US-09-612-914-8

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    Quality: 555.50      Length: 147
    Ratio: 4.480         Gaps: 2
    Percent Similarity: 84.354   Percent Identity: 74.830

alignment_block:
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|||||
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|||||
101 CGGAGACCTGTGCCCTCACCTCGCTGTCTCTGGTGGCTCTGTCACGAGT 150
|||||
34 erGluthrLeuSerLeuThrCysSerValserGlyGlySerIleSerGly 50
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||| :|||
51 AspTyTrpTrpPheTrpIleargGlnSerProGlyLysGlyLeuGluTr 67
|||||
201 GATTGGAGCTACTCTGTTAGTAGTGGGGCCACCAACTACAAACCCGTCCTCC 250
|||||
67 plileGlyTrpIleTyrgLysGlyGlyGlyThrasnTyraasnProSerL 84
|||||
251 TCAAGAGTCGAGTCATCATTTCCACAAGACACAGCTCCAAGAACCAGTTCCTCC 300
||| :|||
84 euAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
|||||
301 CTGAACCTGAACCTCTGTGACCGCCGGGACGCGCGCTGTATTAAGTGTGC 350
|||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrcysAl 117
|||||
351 CAGAGAT .....TGGGCCCAAATAGCTGGAACAACACG 382
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117 aserAsnIleLeuLysTyrrLeuHistrp.....L 127

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seq_documentation_block:
; Sequence 10, Application: US/09612914
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 12, Application US/09612914
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914
; FILING DATE: 10-JUL-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-612-914-12

alignment_scores:
    Quality: 555.50      Length: 147
    Ratio: 4.480         Gaps: 2
    Percent Similarity: 84.354    Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914-12 ..
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1  ATGAACACCTGTGGTTCCTTCCTCCTGGTGGCAGCTCCCGATGGGT 50
|||||
1  MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProargTrpVa 17

51  CTGTGCCCCAGTCACGCTCAGAGAGTCGGGCCAGAGTGGTGAAGCCTT 100
|||||
17  lLeuSerGlnValGlnLeuGlnSerGlyProGlyLeuValtysProS 34

101  CGSAGACCTGTCCTCCCTCACCTGGCTGCTCTCTGTGCTCTGTACAGCAGT 150
|||||
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|||||
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|||||
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; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
;              Newman, Roland A.
;              Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-612-914A-8

alignment_scores:
Quality: 555.50 Length: 147
Ratio: 4.480 Gaps: 2
Percent Similarity: 84.354 Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-8
Align seg 1/1 to: US-09-612-914A-8 from: 1 to: 467
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1 ATGAACACACCTGTGGTTCTTCTCTCTCTGTGGCAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
|||||
51 CTTGTCCACAGCTGAGCTGAGAGTCGGCCCGCAGGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGlnSerGlyProGlyLeuValLysPro 34
|||||
101 CGGAGACCTCTGCCCTCACCTGCTGTCTCTGTGGTGGCTCTGTGACGAGT 150
|||||
34 erGluThrLeuSerLeuThrCysSerValSerValSerGlySerIleSerGly 50
|||||
151 AGTAACCTGTGGACCTGGATCCGCCAGCCCGCAGGGAAGGAGTGGAGTG 200
|| : : :
51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67
|||||
201 GATGACGATATCTCTGGTAGTGTGGTGGGCCACCACTCAACCCGTCCTCC 250
|||||
67 PileGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84
|||||
251 TCAAGAGTCGAGTCATCATTTCAAGACACAGCTCCAAAGAACAGTCTCTCC 300
|| : : :
84 euAsnAsnArgValSerIleAspThrSerLysAsnLeuPheSer 100
|||||
301 CTGAACCTGAACCTGTGTGACCGCGGACGACGCGCGTGTATTACTGTGC 350
|||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117
|||||
351 CAGAGAT.....TGGGCCCAATAAGCTGGAACAACGC 382
| : : :
117 aSerAsnIleLeuLysTyrLeuHisTrp.....L 127

383 TAGGCTTCTGGGCGCAGGAGTCTGTGTCACCGCTCTCTCA 423
|| : : :
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 140

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-10

seq_documentation_block:
; Sequence 10, Application US/09612914A
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
;              Newman, Roland A.
;              Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-612-914A-8

alignment_scores:
Quality: 555.50 Length: 147
Ratio: 4.480 Gaps: 2
Percent Similarity: 84.354 Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-8
Align seg 1/1 to: US-09-612-914A-8 from: 1 to: 467
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; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 467 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-612-914A-10

alignment_scores:
  Quality: 555.50      Length: 147
  Ratio: 4.480        Gaps: 2
  Percent Similarity: 84.354      Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-09-612-914A-10 ..
Align seg 1/1 to: US-09-612-914A-10 from: 1 to: 467

1 ATGAACACCTGGTTCCTCCTCGTGGCCAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCCTCCAGCTGCAGGTGCGGCCCGCCAGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnSerGlyProGlyLeuValLysPros 34
101 CGGAGACCTCTGCTCCCTCACCTGCTGCTGCTGCTGCTGTCAGCAGT 150
|||||
34 erGluthrLeuSerLeuThrCysSerValSerGlySerIleSerGly 50
151 AGTAACCTGGTGGACCTGATCCGCGCCAGCCAGGAGGAGGAGTGGAGTG 200
|||||
51 AspTyrTrpTrpPheTrpPheTrpPheTrpPheTrpPheTrpPheTrp 67
201 GATTGGACGTATCTCTGGTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 250
|||||
67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnProSerL 84
251 TCAAGAGTCGAGTCATCTTTCACAGACACGTCACAGACGTCACAGACGTC 300
|||||
84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
301 CTGAACCTGAACCTCTGTACCGCGCGGACACGCGCGTGTATTACTGTGC 350
|||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117
351 CAGAGAT.....TGGGCCCAAAATAGCTGGAACAACGC 382
| : : :
117 aSerAsnIleLeuLysTyrLeuHisTrp.....L 127
383 TAGGCTTCTGGGGCCAGGAGTCTGCTCACCCTCTCCTCA 423

seq_name: /cgn2_6/ptodata/2/paa/US096_COMB.pep:US-09-612-914A-12
seq_documentation_block:
; Sequence 12, Application US/09612914A
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; Ref, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
```



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101 CGGAGACCCCTGCTCCTACCTGCCTCTCTCTGTGTGGCTGTGTGAGCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysAlaValSerGlyGlySerIleSerGly 50
|||||
151 AGTAAGCTGGTGGACCTGATCCGCCAGCCAGGGAAGGAGGAGTGGAGTG 200
|||||
51 GlyTyrGlyTrpGlyTrpIleArgGlnProProGlyLysGlyLeuGluTr 67
|||||
201 GATTGGACGTATCTCTGTGTGTGGGGCCACCACTACAAACCCGTCCTCC 250
|||||
67 pIleGlySerPheTyrSerSerSerGlyAsnThrTyrTyrAsnProSerL 84
|||||
251 TCAGAGTCGAGTCATCTTTCACAGACAGCTCCAGAACCCAGTTCCTCC 300
|||||
84 euLysSerGlnValThrIleSerThrAspThrSerLysAsnGlnPheSer 100
|||||
301 CTGAACCTGAACCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGC 350
|||||
101 LeuLysLeuAsnSerMetThrAlaAlaAspThrAlaValTyrTyrCysVa 117
|||||
351 CAGAGAT.....TGGGCCCC 364
|||||
117 lArgAspArgLeuPheSerValValGlyMetValTyrAsnAsnTrpPheA 134
|||||
365 AAATAGCTGGACACCTAGGCTTCTGGGGCCAGGAGTCTGTGTGAC 414
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134 spVal.....TrpGlyProGlyValLeuValThr 143
|||||
415 GTCTCTCTCA 423
|||||
144 ValSerSer 146
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seq\_name: /cgn2\_6/ptodata/2/paa/US096\_COMB pep: US-09-612-914-2

## seq\_documentation\_block:

; Sequence 2, Application US/09612914

; GENERAL INFORMATION:

; APPLICANT: Hanna, Nabil

; APPLICANT: Newman, Roland A.

; APPLICANT: Reff, Mitchell E.

; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

; TITLE OF INVENTION: Therapy

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314-3187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/612,914

; FILING DATE: 10-JUL-2000

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/523,894

; FILING DATE: 06-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-165

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 139 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-612-914-2

## alignment\_scores:

Quality: 548.50 Length: 146

Ratio: 4.459 Gaps: 2

Percent Similarity: 84.247 Percent Identity: 73.973

## alignment\_block:

US-09-019-441-2 x US-09-612-914-2

Align seg 1/1 to: US-09-612-914-2 from: 1 to: 139

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1 ATGAACACCTGTGTTCTTCTCTCTGTGTGGCAGTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
|||||
51 CCTGTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 100
|||||
17 lLeuSerGlnValGlnLeuGlnAlaGlyProGlyLeuValLysProS 34
|||||
101 CGGAGACCTGTCCCTCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 150
|||||
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSerGly 50
|||||
151 AGTAACCTGGTGGACCTGATCCGCCAGCCAGGGAAGGAGTGGAGTG 200
|||||
51 AspTyrTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67
|||||
201 GATTGGACGTATCTCTGTGTGTGGGGCCACCACTACAAACCCGTCCTCC 250
|||||
67 pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL 84
|||||
251 TCAGAGTCGAGTCATCTTTCACAGACAGCTCCAGAACCCAGTTCCTCC 300
|||||
84 euAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
|||||
301 CTGAACCTGAACCTCTGTGACCGCGGACACGCGCGTGTATTACTGTGC 350
|||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 117
|||||
351 CAGAGAT.....TGGGCCCAATAAGTGGGAACAACGC 382
|||||
117 aSerAsnIleLeuLysTyrLeuHisTrp.....L 127
|||||
383 TAGGCTTCTGGGGCCAGGAGTCTCTGTGTGCTGCTGCTGCTGCTGCTGCT 420
|||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139
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seq\_name: /cgn2\_6/ptodata/2/paa/US096\_COMB pep: US-09-612-914A-2

## seq\_documentation\_block:

; Sequence 2, Application US/09612914A

; GENERAL INFORMATION:

; APPLICANT: Hanna, Nabil

; APPLICANT: Newman, Roland A.

; APPLICANT: Reff, Mitchell E.

; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human

; TITLE OF INVENTION: Therapy

; NUMBER OF SEQUENCES: 59

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314-3187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/612,914A
; FILING DATE: 10-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/523,894
; FILING DATE: 06-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-612-914A-2
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alignment_scores:
  Quality: 548.50      Length: 146
  Ratio: 4.459        Gaps: 2
  Percent Similarity: 84.247  Percent Identity: 73.973
```

## alignment\_block:

US-09-019-441-2 x US-09-612-914A-2

Align seg 1/1 to: US-09-612-914A-2 from: 1 to: 139

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1 ATGAACACCTGTGGTTCCTCCTCCTGTGGCAGCTCCAGATGGT 50
1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGCCAGGAGTGTGAAGCCTT 100
17 LeuSerGlnValGlnLeuGlnAlaGlyProGlyLeuValLysPro 34
101 CGGAGACCTGTCCCTCACCTGCCTCTCTGTGGTCTGTCTCAGCAGT 150
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerIleSer 50
151 AGTAACCTGGTGGACCTCGATCCGCCAGCCAGGAGGAGGAGTGGAGT 200
51 AspTyrTrpPheTrpIleArgGlnSerProGlyLysGlyLeuGluTr 67
201 GATTGGACGTATCTCTGTAGTGGTGGGCCACCACTACAAACCCGTC 250
67 pIleGlyTyrIleTyrGlySerGlyGlyGlyThrAsnTyrAsnPro 84
251 TCAAGAGTCGAGTCATCATTTCAACAGACACGTCACCAAGAACCGT 300
84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPhe 100
301 CTGAACTGAACTCTGTGACCGCGGACACGCGCGTGTATTACTGTGC 350
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrTyrCys 117
351 CAGAGAT.....TGGGCCCAAAATAGCTGGAACAACGC 382
117 aSerAsnIleLeuLysTyrLeuHisTrp.....L 127
383 TAGCTTCTGGGCCAGGAGTCTCTGTCTACCGTCTCC 420
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139
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seq\_name: /cgn2\_6/ptodata/2/paa/PCURUS\_COMB.pep: PCT-US01-18569-4331

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seq_documentation_block:
; Sequence 4331, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PAI33PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4331
; LENGTH: 193
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (188)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-4331
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alignment_scores:
  Quality: 546.00      Length: 146
  Ratio: 4.368        Gaps: 4
  Percent Similarity: 85.616  Percent Identity: 77.397
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US-09-019-441-2 x PCT-US01-18569-4331

Align seg 1/1 to: PCT-US01-18569-4331 from: 1 to: 193

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6 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpVa 22
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGCCAGGAGTGTGAAGCCTT 100
22 LeuSerGlnValGlnLeuGlnSerGlyProGlyLeuValLysPro 39
101 CGGAGACCTGTCCCTCACCTGCCTCTCTGTGGTCTGTCTCAGCAGT 150
39 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 54
151 AGTAACCTGGTGGACCTCGATCCGCCAGCCAGGAGGAGTGGAGT 200
55 SerTyrTrpTrpSerTrpIleArgGlnProGlyLysGlyLeuGluTr 71
201 GATTGGACGTATCTCTGTAGTGGTGGGCCACCACTACAAACCCGTC 250
71 pIleGlyTyrIleTyrTyrSer...GlySerThrAsnTyrAsnProSer 87
251 TCAAGAGTCGAGTCATCATTTCAACAGACACGTCACCAAGAACCGT 300
87 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 103
301 CTGAACTGAACTCTGTGACCGCGGACACGCGCGTGTATTACTGTGC 350
104 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCys 120
351 CAGA.....GATTGGGCCCAAAATAGCTGGAACAACCGTAG 385
120 aArgGlyProTyrSerSerSerTrpTyrProArgAla...GluTyrPhe 136
386 GCTTCTGGGCCAGGAGTCTCTGTCTACCGTCTCTCTCA 423
136 LnhisTrpGlyGlnGlyThrLeuValThrValSerSer 148
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seq_documentation_block.:
; Sequence 145, Application US/09800729
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

alignment_scores:
Quality: 544.00 Length: 148
Ratio: 4.283 Gaps: 3
Percent Similarity: 85.811 Percent Identity: 74.324

alignment_block:
US-09-019-441-2 x US-09-800-729-145 ..
Align seg 1/1 to: US-09-800-729-145 from: 1 to: 487

1 ATGAACACTGTGTTTCCTCCTCTCTGTGGAGCTCCCAATGGGT 50
1 MetLysHisLeuTrpPheLeuLeuValAlaAProArgTrrVa 17
51 CQTGTCACAGCTGCAGCTGCAGGAGTCGGGCCACAGGAGTGTAAGCCTT 100
17 lueSerGlnValGlnleuGlnGluserglyproglyLeuVallysProS 34
101 CGGAGACCCTGTCCCTCACCTCGCTGTCTCTGTGGCTCTGTGCAGCAGT 150
34 erGluThrLeuSerLeuThrCysThrValSerGlySerIleSer 50
151 ...ACTAACTGGTGACCTGATGATCGCCAGCCCCAGGAAGGACTGGA 197
51 GlyGlyHisTyrrTpSerTrpIleArgGlnHisProGlyLysGlyLeuG1 67
198 GTGGATTGCAGCTATCTCTGGTAGTGTGGGGCCACCACTACACCCGT 247
67 utrIpiledGlyTyrrIleSer...TyrAsnGlyValThrTyrrAsnProS 83
248 CCTCAAGAGTCGAGTCATCATTTTCACAAGACACGTCCCAAGAACCAGTTC 297
83 erLeuLysSerArgvalThrIleSerValaspthrSerGlnAsnGlnPhe 99
298 TCCCTGAACCTGAACCTGTGTGACCGCCGGACACGCGCGTGTATTACTG 347
100 SerLeuArgLeuSerSerValThrAlalaaspThrAlaValTyrrCy 116
348 TGCC.....AGAGATTGGGCCCAAATACTGGAACAA 379
116 saLaLysAsphHisArgAlaThrArgAspGlyTyrrGlnLeuGluTyrrArgg 133
380 CGCTAGGCTTCTGGGGCCAGGAGTCCTGGTGCACCGTCTCTCTCA 423
133 lypHeAspyrrTpGlyGlnGlylleLeuValThrValserSer 147

seq_name: /cgn2_6/podata/2/paa/US098_COMB pep:US-09-833-245-2194

seq_documentation_block:
; Sequence 2194, Application US/09833245
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
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; TITLE OF INVENTION: Albumin Fusion Proteins  
; FILE REFERENCE: PF546PCT  
; CURRENT APPLICATION NUMBER: US/09/833,245  
; CURRENT FILING DATE: 2001-04-12  
; PRIOR APPLICATION NUMBER: 60/229, 358  
; PRIOR FILING DATE: 2000-04-12  
; PRIOR APPLICATION NUMBER: 60/256, 931  
; PRIOR FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 60/199, 384  
; PRIOR FILING DATE: 2000-04-25  
; NUMBER OF SEQ ID NOS: 2267  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2194  
; LENGTH: 487  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-833-245-2194

## alignment\_scores:

Quality: 544.00 Length: 148  
Ratio: 4.283 Gaps: 3  
Percent Similarity: 85.811 Percent Identity: 74.324

## alignment\_block:

US-09-019-441-2 x US-09-833-245-2194 ..

Align seg 1/1 to: US-09-833-245-2194 from: 1 to: 487

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51 CCTGTCCAGCTGCAGCTCAGGAGTCGGCCAGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34
101 CGGAGACCTGTCCCTCACCTGCCTCTCTCTGTGGTGGCTGTGCAGCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSerSer 50
151 ...AGTAACCTGGTGACCTGGATCCGCCAGCCCGCCAGGAGGACTGGA 197
|||||
51 GlyGlyHisTrpSerTrpIleArgGlnHisProGlyLysGlyLeuGl 67
198 GTGGATTGGACGTATCTCTGGTAGTGGTGGGCCACCACTACAACCCGT 247
|||||
67 uTrpIleGlyTyriIleSer...TyrAsnGlyValThrTyrTyrAsnProS 83
248 CCCTCAAGATCGAGTCATCATTTCAAGACAGCTCCACAGACCACTTC 297
|||||
83 erLeuLysSerArgValThrIleSerValAspThrSerGlnAsnGlnPhe 99
298 TCCCTGAACCTGAACCTGTGTACCGCGGACACACGCGCGGTGATTACTG 347
|||||
100 SerLeuArgLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCy 116
348 TGCC.....AGAGATTGGGCCCAATAAGCTGGAACAA 379
|||||
116 sAlaLysAspHisArgAlaThrArgAspGlyTyrGlnLeuGluTyrArgG 133
380 CGCTAGGCTTCTGGGCGCAGGAGTCTCGTCCCGTCTCTCA 423
...
133 lyPheAspTyrTrpGlyGlnGlyIleLeuValThrValSerSer 147
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; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24944
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-24944
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  Quality: 572.00      Length: 146
  Ratio: 4.366        Gaps: 3
  Percent Similarity: 89.726  Percent Identity: 76.027

alignment_block:
US-09-019-441-2 x US-09-791-537-24944 ..
Align seg 1/1 to: US-09-791-537-24944 from: 1 to: 169
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```
1 ATGAACACCTGTGGTCTCTCCTCCTCGTGGCAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpVa 17
|||||
51 CCTCTCCAGCTGCAGTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 34
|||||
101 CGGAGACCTGTCCCTCAGTGCCTCTCTCTGTGGTCTGTGACGAGT 150
|||||
34 erGluThrLeuSerLeuThrCysThrIleSerGlySerIle...Ser 49
|||||
151 AGTAACCTGGTGACCTGGATCGGCCAGCCAGGAGGAGGAGTGGAGTG 200
|||||
50 GlyAspTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66
|||||
201 GATTGGACGTATCTCTGGTAGTGGT.....GGGCCACCA 235
|||||
66 pIleGlyHisIleTyrTrpSerGlyAsnArgTyrThrGlyThrThra 83
|||||
236 ACTACACCCGTCTCCTCAGAGTGCAGTCATCTTCACAGACACGCTCC 285
|||||
83 snTyrAsnProSerLeuLysSerArgValThrIleSerValAspThrSer 99
|||||
286 AAGAACAGATTCTCCCTGAACCTCAACTGTGTGACCGCGGGACACGGC 335
|||||
100 ArgAsnGlnPheSerLeuArgLeuThrSerValThrAlaAlaAspThrAl 116
|||||
336 CGTGTATTACTGTCCAGAGATTGGGCCCAATAAGCTGGAACAACGCTAG 385
|||||
116 aValTyrTyrCysAlaArgGln.....ArgValSerGlyArgAspLeuA 131
|||||
386 GCTTCTGGGCCAGGGAGTCTGTGCTACCGTCTCTCTCA 423
|||||
131 spTyrTrpGlyGlnGlyIleLeuValThrValSerSer 143
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14698
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seq_documentation_block:
; Sequence 14698, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14698
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-14698
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alignment_scores:
  Quality: 570.50      Length: 141
  Ratio: 4.492        Gaps: 2
  Percent Similarity: 90.071  Percent Identity: 80.142
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alignment_block:
US-09-019-441-2 x US-09-791-537-14698 ..
Align seg 1/1 to: US-09-791-537-14698 from: 1 to: 138

1 ATGAACACCTGTGGTCTCTCCTCCTCGTGGCAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpVa 17
|||||
51 CCTGTCCAGCTGCAGTGCAGGAGTGGGCCAGGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 34
|||||
101 CGGAGACCTGTCCCTCAGTGCCTCTCTCTGTGGTCTGTGACGAGT 150
|||||
34 erGluThrLeuSerLeuThrCysAlaValSerGlyTyrSerIle...Ser 49
|||||
151 AGTAACCTGGTGACCTGGATCGGCCAGCCAGGAGGAGGAGTGGAGTG 200
|||||
50 SerAsnTyrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66
|||||
201 GATTGGACGTATCTCTGGTAGTGGGCCACCACTACAACCCGCTCC 250
|||||
66 pIleGlyTyrIleTyrGlySerSerGlySerAlaTyrTyrAsnProSerL 83
|||||
251 TCAAGAGTCAGTCATCTTCACAGACAGCTCCAAAGACCAAGCTTCTCC 300
|||||
83 euLysSerArgValThrIleSerIleAspThrSerLysAsnGlnPheSer 99
|||||
301 CTGAACCTGAACCTGTGACCGCGCGGACAGCGCGCTGTATTACTGTC 350
|||||
100 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 116
|||||
351 CAGAGATTGGGCCCAATAAGCTGGAACAACGCTAGGCTTCTGGGCCAGG 400
|||||
116 aArgAsp.....ProTyrGlyProThrTyrPheAspTyrTrpGlyGlnG 131
|||||
401 GAGTCTGTGTCACCGTCTCTCTCA 423
|||||
131 lyValLeuValThrValSerSer 138
|||||
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14679
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seq_documentation_block:
; Sequence 14679, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; CURRENT APPLICATION NUMBER: US/09/791,537
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14679
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Macaca mulatta
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Length: 141

US-09-019-441-2 x US-09-791-537-89302

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Align seg 1/1 to: US-09-791-537-89302 from: 1 to: 143
1 ATGAACACCTGTGGTCTCTCCCTCTCTGTGGCAGCTCCAGAGCGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 34
101 CGAGAGCCCTGTCCCTCACCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGCCTT 150
|||||
34 erGluThrLeuSerLeuThrCysAlaValSerGlyTyrSerIleSer 50
151 AGTAACCTGGTGGACCTGCATCTCCTCACCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGT 200
|||||
51 GlyTyrGlyTrpAsnTrpIleArgGlnProProGlyLysGlyLeuGluTr 67
201 GATTGGACGTATCTCTGTGTAGTGGTGGGCCCGGAGGAGTGGGCCCGGAGTGGGCCCGTCC 250
|||||
67 pIleGlySerIleGlySerArgGlyAsnThrAsnHisAsnProSerL 84
251 TCAAGAGTCGAGTCATCATCTTCAACAGACAGCTCCCAAGAACCTGCTCC 300
|||||
84 euLysSerArgValThrIleSerIleAspThrSerLysAsnGlnPheSer 100
301 CTGAACCTGAACCTCTGTACCGCGCGGACACAGCTCCCAAGAACCTGCTCC 350
|||||
101 LeuLysLeuArgSerLeuThrAlaAlaAspThrAlaValPheTyrCysAl 117
351 CAGAGATTGGGCCCAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGG 400
|||||
117 aaArgasp...GlyGlyTyrSerSerArgPhePheAspTyrTrpGlyGlnG 133
401 GAGTCTGGTCCAGCTCTCTCTCA 423
133 lyValLeuValThrValSerSer 140
seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14665
seq_documentation_block:
; Sequence 14665, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14665
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Macaca mulatta
US-09-791-537-14665
alignment_scores:
Quality: 566.50 Length: 141
Ratio: 4.461 Gaps: 1
Percent Similarity: 90.071 Percent Identity: 78.723
alignment_block:
US-09-019-441-2 x US-09-791-537-14665
Align seg 1/1 to: US-09-791-537-14665 from: 1 to: 140
1 ATGAACACCTGTGGTCTCTCCCTCTCTGTGGCAGCTCCAGAGCGGT 50
|||||
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```
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysPro 34
101 CGAGAGCCCTGTCCCTCACCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysAlaValSerGlyTyrSerIleSer 50
151 AGTAACCTGGTGGACCTGCATCTCCTCACCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGT 200
|||||
51 GlyTyrGlyTrpAsnTrpIleArgGlnProProGlyLysGlyLeuGluTr 67
201 GATTGGACGTATCTCTGTGTAGTGGTGGGCCCGGAGGAGTGGGCCCGGAGTGGGCCCGTCC 250
|||||
67 pIleGlySerIleGlySerArgGlyAsnThrAsnHisAsnProSerL 84
251 TCAAGAGTCGAGTCATCATCTTCAACAGACAGCTCCCAAGAACCTGCTCC 300
|||||
84 euLysSerArgValThrIleSerIleAspThrSerLysAsnGlnPheSer 100
301 CTGAACCTGAACCTCTGTACCGCGCGGACACAGCTCCCAAGAACCTGCTCC 350
|||||
101 LeuLysLeuArgSerLeuThrAlaAlaAspThrAlaValPheTyrCysAl 117
351 CAGAGATTGGGCCCAATAGCTGGAAACAGCTAGGCTTCTGGGGCCAGG 400
|||||
117 aaArgasp...GlyGlyTyrSerSerArgPhePheAspTyrTrpGlyGlnG 133
401 GAGTCTGGTCCAGCTCTCTCTCA 423
133 lyValLeuValThrValSerSer 140
seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-5239
seq_documentation_block:
; Sequence 5239, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5239
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-5239
alignment_scores:
Quality: 564.00 Length: 150
Ratio: 4.476 Gaps: 3
Percent Similarity: 84.000 Percent Identity: 74.000
alignment_block:
US-09-019-441-2 x US-09-791-537-5239
Align seg 1/1 to: US-09-791-537-5239 from: 1 to: 145
7 CACCTGTGGTCTCTCCCTCTCTGTGGCAGCTCCAGAGTGGTGGTCTGTC 56
|||||
1 HisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpValLeu 17
57 CCAGCTGCAGTGCAGGAGTGGGCCCGGAGGAGTGGTGAAGCCTTCGGAGA 106
|||||
17 rGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProSerGlyT 34
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251 TCAAGAGTCGAGTCATCATTTTCAAGAAGACACGTCCTCAAGAACCAGTTCCTCC 300  
 |||||  
 |||||  
 82 euLysSerArgValThrMetSerValAspMetSerLysAsnGlnPheSer 98  
 |||||  
 |||||

```
301 CTGAACCTGAACCTGTGACCGCGCGACACGCGCTGTATTACTGTGC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 LeuAsnLeuAsnSerValThrAlaAlaAspThrAlaValTyrCysAl 115
351 CAGAGATTGGGCCCAATAGCTGGAACA...AGCTAGGCTTCTGGGGCC 397
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
115 aArgGlyProLysThrLeuAlaGlyThrSerSerPheAsnTrpGlyG 132
398 AGGAGTCTGTCACGCTCCTCA 423
|||||:|||||:|||||:|||||:|||||:|||||:
132 InGlyThrLeuValThrValSer 140
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-16932

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seq_documentation_block:
; Sequence 16932, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16932
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-16932
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  Quality: 558.00      Length: 145
  Ratio: 4.359        Gaps: 3
Percent Similarity: 88.276  Percent Identity: 76.552

alignment_block:
US-09-019-441-2 x US-09-791-537-16932  ..
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Align seg 1/1 to: US-09-791-537-16932 from: 1 to: 144

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1 MetLysHisLeuTrpPheLeuLeuValAlaAlaProArgTrpVa 17
51 CTTGTCCACGCTGCAGTCGAGAGTCGGCGCCAGGAGTGGTGAAGCCTT 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 LeuSerGlnValGlnLeuGlnSerGlyProGlyLeuValLysPro 34
101 CGGAGACCTGTCCCTCACCTCGCTCTCTGTGGTCTGTGCAGCAGT 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 49
151 AGTAACCTGGTGACCTGGATCCGCCAGCCCCCAGGGAAGGACTGGAGTG 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr 66
201 GATTGGACGTATCTGTGGTGTGGTGGGGCCACCACTACACCCGTCCTCC 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL 82
251 TCAAGAGTCGAGTCATCTTTCACACACACGTCCTCAAGAACCACTCTCC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
82 eulysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer 98
301 CTGAACCTGAACCTGTGACCGCGCGACACGCGCTGTATTACTGTGC 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrCysAl 115
```

```
351 CAGAGATTGGGCCCAATAGCTGGAACAACGCTA.....GGCT 388
|||||:|||||:|||||:|||||:|||||:|||||:
115 aArgAsnTyrTyrAspSerSerGlyTyrArgMetAspTyrTyrPheAspT 132
389 TCTGGGGCCACAGGAGTCTCTGGTCACCGTCTCTCTCA 423
|||||:|||||:|||||:|||||:|||||:|||||:
132 yrTrpGlyGlnGlyThrLeuValThrValSerSer 143
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Sequence	Strd Orig	ZScore	EScore	Len	! Documentation
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/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-523-894-8	+	555.50	996.02	1.2e-48
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-523-894-10	+	555.50	996.02	1.2e-48
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-523-894-12	+	555.50	996.02	1.2e-48
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/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-487-039-108	+	548.50	995.85	4.0e-48
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-476-349A-108	+	548.50	995.85	4.0e-48
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-523-894-2	+	548.50	995.85	4.0e-48
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-487-550-4	+	524.50	939.10	1.7e-45
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-08-480-774A-2	+	519.50	942.57	3.6e-45
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-114	+	518.50	942.76	4.3e-45
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-142	+	518.00	941.76	4.8e-45
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-140	+	514.00	934.61	1.2e-44
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-123	+	513.00	932.61	1.6e-44
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-92	+	510.00	927.30	3.1e-44
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-137	+	493.00	895.84	1.7e-42
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-116	+	490.00	890.52	3.4e-42
/cgn2_6/ptodata/2/1aa/6A_COMB.p	pep:US-08-545-809A-118	+	488.00	887.04	5.5e-42
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-259-372A-6	+	477.50	866.33	6.7e-41
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-488-671-6	+	477.50	866.33	6.7e-41
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-09-260-527-3	+	460.00	836.69	5.2e-39
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-09-025-769B-25	+	457.00	830.14	7.9e-39
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-09-025-769B-39	+	456.50	829.14	8.9e-39
/cgn2_6/ptodata/2/1aa/6B_COMB.p	pep:US-09-025-769B-65	+	456.50	829.14	8.9e-39
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-478-039-80	+	456.50	828.97	9.0e-39
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-476-349A-80	+	456.50	828.97	9.0e-39
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-137-117D-69	+	455.50	825.76	1.2e-38
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-08-436-717-69	+	455.50	825.76	1.2e-38
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-478-039-76	+	449.00	814.90	5.3e-38
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-476-349A-76	+	449.00	814.90	5.3e-38
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-478-039-78	+	447.50	812.24	7.5e-38
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-476-349A-78	+	447.50	812.24	7.5e-38
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-137-117D-64	+	443.50	805.01	1.9e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-08-436-717-64	+	443.50	805.01	1.9e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-08-360-125-11	+	441.00	800.52	3.4e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-08-360-125-11	+	441.00	800.52	3.4e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-08-450-578-11	+	441.00	800.52	3.4e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-09-017-628-11	+	441.00	800.52	3.4e-37
/cgn2_6/ptodata/2/1aa/5B_COMB.p	pep:US-09-014-880-11	+	441.00	800.52	3.4e-37
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-918-148-79	+	432.00	776.82	3.6e-36
/cgn2_6/ptodata/2/1aa/5A_COMB.p	pep:US-08-478-039-77	+	431.00	782.48	3.5e-36



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; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-523-894-12

alignment_scores:
    Quality: 555.50      Length: 147
        Ratio: 4.480          Gaps: 2
Percent Similarity: 84.354   Percent Identity: 74.830

alignment_block:
US-09-019-441-2 x US-08-523-894-12 ..

Align seg l/1 to: US-08-523-894-12 from: 1 to: 467

1 ATGAACACTCTGTGTTTCCTCCCTGGTGCAGCTCCCAGATGGGT 50
|||||
1 MetLysHisLeutrPheLeuValAlaIleProargTrpVa 17

51 CCTGTCCCCAGCTGCAGCTCAGGAGTCGGGCCCGCAGGAGTGTAAGCCTT 100
|||||
17 lleuSerGlnValGlnLeuGlnGlusErGlyProGlyLeuVallysPros 34

101 CGGAGACCCTGTCCTCACTCGCTGCCTCTCTGGTGGCTCTGTCAAGCAT 150
|||||
34 erGLUThrLeuSerLeuThrCysSerValserGlyGlySerlleSerGly 50

151 AGTAACTGGTGACCTGGATCCGCCAGCCCCCGAAGGAGGACTGGAGTG 200
||| :||| |||||
51 AspTyrtyrtrrPhetrprileargLnSerProglyltylsGlyLeuGluIr 67

201 GATTGGACGTATCTCTGGTAGTGGTGGGGCCACCAACTACAACCCGTCCT 250
||||| |||
67 pilegLyTYrlleTyrgLYserGlyGlyThrasnTyAsnPaserL 84

251 TCAAGAGTCGAGTCATCATTTACAAGACACAGCTCCAAGAACCATCTTCC 300
||||| :|||
84 euASnArGValSeriIlSeRilEasOthrSerlyvsnLeuPheser 100
```



```
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 108:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-478-039-108

alignment_scores:
  Quality: 548.50      Length: 146
  Ratio: 4.459        Gaps: 2
  Percent Similarity: 84.247      Percent Identity: 73.973

alignment_block:
  US-09-019-441-2 x US-08-478-039-108
  Align seg 1/1 to: US-08-478-039-108 from: 1 to: 139

1 ATGAACACCTGTGTTCTCCTCCTCCTGTCGTCAGTCCAGATGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGTCGTCAGTGCAGGAGTCGGGCCAGAGTGGTGAAGCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnAlaGlyProGlyLeuValLysProS 34
101 CGGAGACCTGTCCCTCCTCCTCCTCCTCCTGTCGTGTCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysSerValSerGlyGlySerGly 50
151 AGTAACCTGGTGGACCTGTGTCGTCAGTCCAGCCAGGAGGAGTGGAGTG 200
|||||
51 AspTyrTrpPheTrpPheTrpPheTrpPheTrpPheTrpPheTrp 67
201 GATTGGACGTATCTCTCTGTCAGTGGTGGGCCACCACTACAAACCCGTC 250
|||||
67 pIleGlyTyrIleTyrGlySerGlyGlyThrAsnTyrAsnProSerL 84
251 TCAGAGTCGAGTCATCATTTTCACACACAGTCCTCAGAACCACTTCTCC 300
|||||
84 euAsnAsnArgValSerIleSerIleAspThrSerLysAsnLeuPheSer 100
301 CTGAACCTGAACTCTGTGACCGCGCGACACAGCGCGTGTATTACTGTGC 350
|||||
101 LeuLysLeuArgSerValThrAlaAlaAspThrAlaValTyrCysAl 117
351 CAGAGAT.....TGGGCCAAATAGCTGGAACAACGC 382
|||||
117 aserAsnIleLeuLysTyrLeuHisTrp.....L 127
383 TAGGCTTCTGGGGCCAGGAGTCTCTGTCACCGTCTCC 420
|||||
127 euLeuTyrTrpGlyGlnGlyValLeuValThrValSer 139

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-476-349A-108

seq_documentation_block:
; Sequence 108, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabli
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
```



MOLECULE TYPE: protein  
US-08-487-550-4

alignment\_scores:  
Quality: 524.50 Length: 146  
Ratio: 4.264 Gaps: 2  
Percent Similarity: 84.247 Percent Identity: 71.233

alignment\_block:

US-09-019-441-2 x US-08-487-550-4 ..

Align seg 1/1 to: US-08-487-550-4 from: 1 to: 476

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1 ATGAACACCTGGTGGTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT 50
|||||
1 MetIshisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTT 100
|||||
17 LeuSerGlnValIleuGlnTrpGlyGluGlyLeuGlnProS 34
101 CGGAGACCTGTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 150
|||||
34 erGluThrLeuSerArgThrCysValValSerGlyGlySerIleSerGly 50
151 AGTAACCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 200
|||||
51 TyrTyrTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTrpTr 67
201 GATTGGACGTATCTCTGCTAGTGGTGGGCCACCACTACAAACCGTCC 250
|||||
67 PileGlyHisIleTyrGlyAsnGlyAlaThrThrAsnTyrAsnProSerL 84
251 TCAAGAGCTCGAGTCATCATTTCAACAGACACGCTCCCAAGAACCTCC 300
|||||
84 eulysSerArgValThrIleSerLysAspThrSerLysAsnGlnPhePhe 100
301 CTGAACTGAACCTCTGTGACCGCGCGGACACGCGCGCTGTATTACTG 350
|||||
101 LeuAsnLeuAsnSerValThrAspAlaAspThrAlaValTyrTyrCysAl 117
351 CAGA.....GATTGGGCCCAAAATAGCT...GGAACAACGCTAG 385
|||||
117 aaRGlyProArgProAspCysThrThrIleCysTyrGlyTrpVala 134
386 GCTTCTGGGGCAGGAGTCTCTGCTCCTCCTCCTCCTCCTCA 423
|||||
134 spValTrpGlyProGlyAspLeuValThrValSerSer 146
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seq\_name: /cqn2\_6/ptodata/2/1aa/5B\_COMB.pap:US-08-480-774A-2

seq\_documentation\_block:

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; Sequence 2, Application US/08480774A
; Patent No. 5852186
; GENERAL INFORMATION:
; APPLICANT: MARASCO, Wayne A.
; APPLICANT: SODROSKI, Joseph G.
; APPLICANT: HASELTINE, William A.
; APPLICANT: POSNER, Marshall R.
; TITLE OF INVENTION: REACTIVE NEUTRALIZING HUMAN
; TITLE OF INVENTION: ANTI-gp 120 RECOMBINANT ANTIBODY, DNA CODING THE SAME
; TITLE OF INVENTION: AND USE THEREOF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
; STREET: 130 Water Street
; City: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,774A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/400,674
; FILING DATE: 08-MAR-1995
; APPLICATION NUMBER: 07/804,652
; FILING DATE: 10-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Resnick, David S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41450-FWC-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-480-774A-2
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alignment\_scores:  
Quality: 519.50 Length: 150  
Ratio: 4.190 Gaps: 4  
Percent Similarity: 82.667 Percent Identity: 71.333

alignment\_block:

US-09-019-441-2 x US-08-480-774A-2 ..

Align seg 1/1 to: US-08-480-774A-2 from: 1 to: 142

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1 ATGAACACCTGGTGGTTCCTCCTCCTGGTGGCAGCTCCAGATGGGT 50
|||||
1 MetGluHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17
51 CCTGTCCAGCTGCAGCTGCAGGAGTCGGGCCAGGAGTGTGAAGCCTT 100
|||||
17 LeuSerGlnValGlnLeuGlnGluSerGlyProGlyLeuValLysProS 34
101 CGGAGACCTGTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTC 150
|||||
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 49
151 AGTAACCTGGTGGACCTGCATCCGCCACCCAGGAGGAGGAGTGGAGTG 200
|||||
50 SerHisTyrTrpSerTrpIleArgGlnSerProGlyLysGlyLeuGlnTr 66
201 GATTGGACGTATCTCTGCTAGTGGTGGGCCACCACTACAAACCGTCC 250
|||||
66 PileGlyTyrIleTyrTrpSer...GlySerThrAsnTyrSerProSerL 82
251 TCAAGAGCTCGAGTCATCATTTCAAGACACACGCTCCAAAGAACCTGTC 300
|||||
82 eulysSerArgValThrIleSerValGluThrSerLysAsnGlnPheSer 98
301 CTGAACCTGAACCTCTGTGACCGCGCGGACACGCGCGCTGTATTACTG 350
|||||
99 LeuLysLeuThrSerMetThrAlaAlaAspThrAlaValTyrTyrCysAl 115
351 CAGA.....GATTGGGCCCAAAATAGCT...GATTGGGCCCAAAATAGCTG 373
|||||
115 aaRGlyProValProAlaValPheTyrGlyAspTyr..... 127
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; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-140

alignment_scores:
    Quality: 514.00      Length: 118
    Ratio: 4.673        Gaps: 2
    Percent Similarity: 93.220    Percent Identity: 86.441

alignment_block:
US-09-019-441-2 x US-08-545-809A-140    ..

Align seg 1/1 to: US-08-545-809A-140 from: 1 to: 116

1 ATCAACACCTGTGGTTCCTCTCTCTGTGGCAGCTCCAGATGGGT 50
|||||
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAaProArgTpvA 17
|||||
51 CCTGTCCCAGCTCAGCTGCAGAGTGGGGCCAGGAGTGGTGAAGCCTT 100
|||||
17 lLeuSerGlnValGlnLeuGlnSerGlyProGlyLeuVallyProS 34
|||||
101 CGGAGACCCTGTCCCTCACCTGCCTGTCTGTGGTGGCTGTGCAGCAGT 150
|||||
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerVal...Ser 49
|||||
151 AGTAACCTGGTGACCTGGATCCGCCACGCCCCAGGGAAGGACTCGAGT 200
|||||
50 SerTyrtYrTrpSerTrpIleArgGlnProProGlyLysGlyLeuGluTr 66
|||||

```

[illegible]

```

00 preeglytylilleytylser...glysermlasmyrlnsrposeld 02
251 TCAAGAGTCGAGTCATCATTTTCAAGACACAGCTCCAGAACACAGTCTCC 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
82 euLysSerArgValThrIleSerValAspThrSerLysAsnGlnPheSer 98
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
301 CTGAACCTGAACCTCTGTGACCGCGCGGACGACGCGCTGTATTACTGTCC 350
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
99 LeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCysAl 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
351 CAGA 354
      ||||
115 aaarg 116

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-123

seq_documentation_block:
; Sequence 123, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

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seq name: /cqn2 6/ptodata/2/iaa/6A COMB. pep: US-08-545-809A-123

APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-8906  
TELEFAX: 617-542-5070  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 123:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 118 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-123

alignment\_scores:  
Quality: 513.00 Length: 119  
Ratio: 4.664 Gaps: 2  
Percent Similarity: 92.437 Percent Identity: 85.714

alignment\_block:  
US-09-019-441-2 x US-08-545-809A-123 ..

Align seg 1/1 to: US-08-545-809A-123 from: 1 to: 118

1 ATGAACACCTGTGGTCTCTCCCTGCTGCGAGCTCCAGATGGGT 50  
|||||  
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
51 CTGTGCCAGCTGCAGTCGAGAGTCGGGCCCGCAGGAGTGGTGAAGCCTT 100  
|||||  
17 LeuSerGlnLeuGlnLeuGlnSerGlyProGlyLeuVallyPros 34  
101 CGAGAGCCCTGTCCTCCACCTGCTGCTCTCTGCTGCTGTCGACGAGT 150  
|||||  
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIleSer 50  
151 AGTAAC...TGGTGGACCTGATCCGCGCAGCCCGCAGGGAAGGAGTGGGA 197  
|||||  
51 SerSerTyrTyrTrpGlyTrpIleArgGlnProProGlyLysGlyLeuG 67  
198 GTGGATGGACGATCTCTGCTGATGCTGGTGGGCCCGCAGCAGTCAACCCGT 247  
|||||  
67 utpIleGlySerIleTyrTrpSer...GlySerThrTyrTyrAsnPros 83  
248 CCTCAAGAGTCGAGTCATCATTTCAACAGACACGCTCCAGAACCGTTC 297  
|||||  
83 erLeuLysSerArgValThrIleSerValAspThrSerLysAsnGlnPhe 99  
298 TCCTGAACTGAACTGTGTGACCGCGCGCAGCAGCCCGTGTATTACTG 347  
|||||  
100 SerLeuLysLeuSerSerValThrAlaAlaAspThrAlaValTyrTyrCy 116  
348 TGCAGCA 354  
|||||  
116 sAlaArg 118

seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB pep: US-08-545-809A-92

seq\_documentation\_block:  
Sequence 92, Application US/08545809A  
Patent No. 6096878  
GENERAL INFORMATION:  
APPLICANT: Honjo, Tasuku  
APPLICANT: Matsuda, Fumihiko  
TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE

TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME  
NUMBER OF SEQUENCES: 145  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/00603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 92:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-92

alignment\_scores:  
Quality: 510.00 Length: 118  
Ratio: 4.636 Gaps: 2  
Percent Similarity: 93.220 Percent Identity: 84.746

alignment\_block:  
US-09-019-441-2 x US-08-545-809A-92 ..

Align seg 1/1 to: US-08-545-809A-92 from: 1 to: 116

1 ATGAACACCTGTGGTCTCTCCCTGCTGCGAGCTCCAGATGGGT 50  
|||||  
1 MetLysHisLeuTrpPhePheLeuLeuValAlaAlaProArgTrpVa 17  
51 CTGTGCCAGCTGCAGTCGAGAGTCGGGCCCGCAGGAGTGGTGAAGCCTT 100  
|||||  
17 LeuSerGlnValGlnLeuGlnSerGlyProGlyLeuVallyPros 34  
101 CGAGAGCCCTGTCCTCCACCTGCTGCTCTCTGCTGCTGTCGACGAGT 150  
|||||  
34 erGluThrLeuSerLeuThrCysThrValSerGlyGlySerIle...Ser 49  
151 AGTAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 200  
|||||  
50 SerTyrTyrTrpSerTrpIleArgGlnProAlaGlyLysGlyLeuGluTr 66  
201 GATTGGACGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 250  
|||||  
66 pIleGlyArgIleTyrThrSer...GlySerThrAsnTyrAsnProSerL 82  
251 TCAAGAGTCGAGTCATCATTTCAACAGACACGCTCCAGAACCGAGTTC 300  
|||||  
82 euLysSerArgValThrMetSerValAspThrSerLysAsnGlnPheSer 98  
301 CTGAACCTGAACTCTGTGACCGCGCGGACACGCGCTGATTACTGTGC 350  
|||||

OM of: US-09-019-441-3 to: PIR\_71.\* out\_format : pfs  
Date: Sep 23, 2002 10:02 AM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
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-DB=PIR\_71 -QFMT=fastan -SUFFIX=rpr -GAPOP=12.000 -GAPEXT=4.000  
-MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500  
-OGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000  
-FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500 -DELOP=6.000  
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0  
-ALIGN=15 -MODE=LOCAL -OUTFT=pfs -NORM=ext -HEAPSIZE=500  
-MINLEN=0 -MAXLEN=200000000 -USER=US09019441 @CGN1\_1.227  
-NCPU=6 -ICPU=3 -LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30  
-NO\_XLPXY -WAIT -THREADS=1

## Search information block:

Query: US-09-019-441-3  
Query length: 387  
Database: PIR\_71.\*  
Database sequences: 283138  
Database length: 96089334  
Search time (sec): 132.110000

## score\_list:

Sequence	Strd	Orig	ZScore	EScore	Len	Documentation
pir2:S52793	+	588.00	934.06	4.8e-44	129	Ig kappa chain V region - human
pir2:S40331	+	586.00	931.19	7.2e-44	129	Ig kappa chain - human
pir2:S40317	+	586.00	930.90	7.2e-44	129	Ig kappa chain - human
pir2:S40367	+	578.00	918.34	3.6e-43	129	Ig kappa chain V-J-C region - human
pir1:K1HUKK	+	578.00	918.24	3.6e-43	129	Ig kappa chain precursor V-I region - human
pir2:S38646	+	571.00	907.02	1.5e-42	132	Ig kappa chain V region - human
pir2:S40334	+	571.00	907.02	1.5e-42	132	Ig kappa chain - human
pir2:S52792	+	569.00	904.00	2.3e-42	129	Ig kappa chain V region - human
pir2:S46378	+	565.00	897.72	5.1e-42	128	Ig light chain variable region - human
pir2:S52789	+	564.00	896.09	6.2e-42	129	Ig kappa chain V region - human
pir2:S40333	+	559.00	888.38	1.7e-41	125	Ig kappa chain V-J region - human
pir2:S42066	+	557.00	885.62	2.6e-41	117	Ig kappa chain V region (Vx O12)
pir2:S49134	+	554.00	879.72	4.6e-41	141	Ig kappa chain V-I region (ISE)
pir2:S40352	+	553.00	878.59	5.8e-41	131	Ig kappa chain V-J-C region - human
pir2:S11240	+	548.00	870.88	1.6e-40	127	Ig kappa chain V region - human
pir2:S40313	+	545.00	866.33	3.0e-40	123	Ig kappa chain V-J region - human
pir2:S27524	+	542.00	861.94	5.5e-40	116	Ig kappa chain precursor V-I region - human
pir2:S42284	+	542.00	861.89	5.5e-40	117	Ig kappa chain V region (L11)
pir2:S40314	+	541.00	860.05	6.7e-40	122	Ig kappa chain - human
pir2:S40335	+	538.00	855.10	1.2e-39	126	Ig kappa chain V-J-C region - human
pir2:S41809	+	537.00	853.98	1.5e-39	117	Ig kappa chain V region A30 - human
pir2:S40336	+	535.50	851.25	2.0e-39	124	Ig kappa chain V-J region - human
pir2:S40349	+	535.00	850.41	2.2e-39	125	Ig kappa chain V-J region - human
pir2:S40369	+	535.00	850.21	2.2e-39	129	Ig kappa chain - human
pir2:S40370	+	534.00	848.97	2.8e-39	122	Ig kappa chain - human
pir2:S40318	+	532.00	845.71	4.1e-39	134	Ig kappa chain precursor - human
pir2:S24320	+	530.00	842.02	6.1e-39	135	Ig kappa chain precursor V-I region - human
pir2:S21527	+	528.00	839.74	9.4e-39	117	Ig kappa chain precursor V-I region - human
pir2:S40368	+	527.00	837.51	1.1e-38	130	Ig kappa chain - human
pir2:S40333	+	525.00	834.59	1.7e-38	125	Ig kappa chain V-J-C region - human
pir1:K1HUII	+	524.00	832.81	2.1e-38	129	Ig kappa chain precursor V-I region - human
pir1:K1HUI2	+	521.00	828.67	3.9e-38	117	Ig kappa chain precursor V-I region - human
pir2:S42263	+	520.00	827.08	4.8e-38	117	Ig kappa chain V region (08) - human
pir2:S40315	+	518.50	824.30	6.4e-38	125	Ig kappa chain - human
pir2:S10227	+	518.00	823.92	7.2e-38	117	Ig kappa chain precursor V region - human
pir2:S41810	+	514.00	819.17	1.3e-37	117	Ig kappa chain V region L14 - human
pir2:S43528	+	514.00	817.59	1.6e-37	117	Ig kappa chain V region (018) - human
pir2:S11700	+	513.00	816.01	2.0e-37	117	Ig kappa chain precursor V-I region - human
pir2:S24207	+	513.00	816.01	2.0e-37	117	Ig kappa chain V region (Vx 014)
pir2:S40348	+	513.00	815.65	2.0e-37	124	Ig kappa chain V-J region - human

pir2:S40316 + 513.00 815.60 2.0e-37 125 ! Ig kappa chain - human  
pir2:S40350 + 513.00 815.60 2.0e-37 125 ! Ig kappa chain - human  
pir2:S46376 + 510.00 811.26 3.6e-37 117 ! Ig kappa chain V-J region (T  
pir2:S41814 + 508.00 808.10 5.5e-37 117 ! Ig kappa chain V region (L23  
pir2:S21668 + 507.00 806.52 6.7e-37 117 ! Ig kappa chain V region (24)

seq\_name: pir2:S52793

## seq\_documentation\_block:

Ig kappa chain V region - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
C:Accession: S52793  
R:Rocca, A.; Khamilichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Der  
submitted to the EMBL Data Library, March 1995  
A:Description: Light chain V region gene usage restriction and peculiarities in myelo  
A:Reference number: S52789  
A:Accession: S52793  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-129 <ROC>  
A:Cross-references: EMBL:X85997; NID:g758600; PIDN:CAAS9989.1; PID:g758601  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:38-112/Domain: immunoglobulin homology <IMM>

## alignment\_scores:

Quality: 588.00 Length: 129  
Ratio: 4.820 Gaps: 0  
Percent Similarity: 94.574 Percent Identity: 88.372

## alignment\_block:

US-09-019-441-3 x S52793

Align seg 1/1 to: S52793 from: 1 to: 129

1 ATGCACATGAGGTCCTCCGGCTCAGCTCCTCTGGGGCTCTCTTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17  
51 CCCAGGTGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100  
|||||  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34  
101 CTGCATCTGTAGGGGACAGATGACCATCATCTTCAGGGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsn 50  
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAACCCAGGAAAGCTCTTAA 200  
|||||  
51 IleIleSerTyLeuAsnTrpTyGlnGlnIysProGlyLysAlaProLy 67  
201 GTCCTCATCTATCTGCATCCAGTTCGAAAGTGGGTGCCATCAAGGT 250  
|||||  
67 sLeuLeuMetTyAlaAlaSerSerLeuGlnSerGlyValProAlaArgP 84  
251 TCAGCGCAGTGGATCTGGGACAGAGTTCATCTCACCCTCAGCAGCGTG 300  
heValGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTTGGCAGTATTACTGTCTACAGTTTATAGTACCCC 350  
|||||  
101 GlnProGlnAspPheAlaThrTyTyCysGlnGlnThrTySerAlaPr 117  
351 TCGGACGTCTGGCCCAAGGACCAAGGTGGAAATCAAA 387  
117 oLeuThrPheGlyGlyThrLysValGluIleLys 129

seq\_name: pir2:S40331

## seq\_documentation\_block:

Ig kappa chain - human

C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40331  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40331  
A>Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-123 <KLE>  
A:Cross-references: EMBL:X72441; NTD:9441350; PIDN:CAN51109.1; PID:9441351  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotrimer; immunoglobulin  
F:32-106/Domain: immunoglobulin homology <IMM>

```
alignment_scores:
  Quality: 586.00
  Ratio: 4.966
  Percent Similarity: 95.935
  Length: 123
  Gaps: 0
  Percent Identity: 92.683
```

alignment\_block:  
US-09-019-441-3 x S40331

Align seg 1/1 to: S40331 from: 1 to: 123

19 GCTCAGCTCTCTGGGCTCCTTCTGCTCTGGCTCCAGGTCACGATGTGA 68  
1 AlaGlnLeuLeuGlyLeuLeuLeuLeuLeuTrpLeuArgGlyAlaArgCysAs 17  
69 CATCCAGATGACCCAGTCTCCATCTCTCCCTCTCTGCACTCTAGGGGACA 118  
17 pIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAspA 34  
119 GAGTCACCATCACTTTCGAGGGCAAGTCAGGACCATTAGTATTATTTAAAT 168  
34 rgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuAsn 50  
169 TGGTATCAGCAGAACACCGAGGAAGCTCTTAAGCTCTCTGATCTATGTGC 218  
51 TrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAlaAl 67  
219 ATCCAGTTTGCAAGTGGGGTGCCCATCAAGGTTTCAGCGCAGGTGGATCTG 268  
67 aSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySerG 84  
269 GCACAGAGTTCACTCTACCCCTCAGCAGCCTGCAGCCTGAAGATTTTGGG 318  
84 lyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheAla 100  
319 ACTTATTACTCTCAACAGGTTTATAGTACCCTTCGACAGCTTCGGCCCAAG 368  
101 ThrTyrTyrCysGlnGlnSerTyrSerThrProArgThrPheGlyGlnG 117  
369 GACCAAGTGGAAATCAA 387  
117 yThrLysValGluIleLys 123

seq\_name: pir2:S40317

```

seq_documentation_block:
  Ig kappa chain - human
  C:Species: Homo sapiens (man)
  C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
  C:Accession: S40317
  R:Klein, R.; Jaenichen, R.; Zachau, H.G.
  Eur. J. Immunol. 23, 3248-3271, 1993
  A:title: Expressed human immunoglobulin chi genes and their hypermutation.
  A:Reference number: S40312; MUID:94080891
  A:Accession: S40317
  A:Status: preliminary; translation not shown
  A:Molecule type: mRNA

```

A; Residues: 1-129 <KLE>  
A; Cross-references: EMBL:X72427; NID:G441322; PID:CAA51095.1; PID:G441323  
C; Superfamily: immunoglobulin V region; immunoglobulin homology  
C; Keywords: heterotetramer; immunoglobulin  
F:37-111/Domain: immunoglobulin homology <IMM>

alignment_scores:		
Quality:	586.00	Length: 128
Ratio:	4.843	Gaps: 0
Percent Similarity:	94.531	Percent Identity: 89.062

alignment\_block:

US-09-019-441-3 x S40317

Align seg 1/1 to: S40317 from: 1 to: 129

4 GACATGAGGGTCCCGCTCCTCCTCCTGGGGCTCCTTCTGCTCTGGCTCCC 53  
1 AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuAr 17  
54 AGGTGCCAGATGTGACATCCAGATCACCAGCTCCATCTTCCCTGCTCG 103  
17 gGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSer 34  
104 CATCTGTAGGGGACAGAGTCCACCATCTACTTCGAGGCCAAGTCAGGACATT 153  
34 hrSerLeuGlyAspArgValThrIleThrCysArgAlaSerGlnSerIle 50  
154 AGGTATTATTAAATTCGTATCAGCAGAAACCCAGAAAAGCTCCTAAGCT 203  
51 GlyThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLysP 67  
204 CCTGATCATGTTGCATCCAGTTTGCAAGTGGGTCCCATCAAGGTTCA 253  
67 eLeuIleTyrGlyAlaSerSerLeuGlnSerGlyValProSerArgPheS 84  
254 GCGGCATGATCTGGGACAGACAGTTCACTCTCACCGTCAGCAGCTCGAG 303  
84 erGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGln 100  
304 CCTGAAGATTTGGCACTATTACTGTCTCAGAGGTTTATAGTACCCCTCG 353  
101 ProGluAspPheAlaThrTyrTyrCysGlnGlnThrTyrSerThrProPr 117  
354 GAGCTTCGGCCAGGGACCAAGGTGGAATCAA 387  
117 oThrPheGlyGlyThrLysValGluIleLys 128

seq\_name: pir2:S40367

```

seq_documentation_block:
  lg_kappa_chain_V-J-C_region - human
  C:Species: Homo sapiens (man)
  C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
  C:Accession: S40367
  R:Klein, R.; Jaenichen, R.; Zachau, H.G.
  Eur. J. Immunol. 23, 3248-3271, 1993
  A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
  A:Reference number: S40312; MUID:94080891

```

```
alignment_scores:
  Quality: 578.00
  Ratio: 4.898
  Length: 124
  Gaps: 0
```

1110/Disulfide bonds: #status predicted

Align seg 1/1 to: S38646 from: 1 to: 132

```

1  ATGCATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGCTGCTGCT 50
|||||
3  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTprLe 19
|||||
51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
19  uProGlyAlaArgCysAlaIleArgIleAlaGlnSerProSerSerLeuS 36
|||||
101  CTGCATCTGTAGGGGACAGAGTCCACCTCCTGCAGGGCAAGTCAGGAC 150
|||||
36  erAlaSerThrGlyAspArgValThrIleThrCysArgAlaSerGlnGly 52
|||||
151  ATTAGGTATTATTAAATTTGGTATCAGCAGAAACAGGAAAAGCTCCTAA 200
|||||
53  IleSerSerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 69
|||||
201  GCTCTGATCTATGTGATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
|||||
69  sLeuLeuIleTyrAlaAlaSerThrLeuGlnSerGlyValProSerArgp 86
|||||
251  TCAGCGCAGTGGATCTGGGACAGATTCACCTCACCCTCAGCAGCGTG 300
|||||
86  heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerCysLeu 102
|||||
301  CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
103  GlnSerGluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerTyrPr 119
|||||
351  TCGCAGCTTCGGGCAAGGGACCAAGGTGGGAATCAAA 387
|||||
119  oArgThrPheGlyGlnGlyThrLysValGluIleLys 131

```

seq\_name: pir2:S40334

seq\_documentation\_block:

```

Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40334
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur.J. Immunol. 23, 3248-3271, 1993
A:title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40334
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-132 <KLE>
A:Cross-references: EMBL:X72444
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

```

alignment\_scores:

```

Quality: 571.00 Length: 128
Ratio: 4.839 Gaps: 0
Percent Similarity: 92.188 Percent Identity: 86.719

```

alignment\_block:

US-09-019-441-3 x S40334 ..

Align seg 1/1 to: S40334 from: 1 to: 132

```

4  GACATGAGGTGCCCGCTCAGCTCCTGGGCTCCTCTGCTGCTGCTCCC 53
|||||
1  AspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLeuPr 17
|||||
54  AGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTG 103
|||||
17  oglyAlaArgCysAspIleGlnLeuThrGlnSerProSerPheLeuSera 34
|||||

```

```

104  CATCTGTAGGGGACAGAGTCCACCTCAGCTTCAGGGCAAGTCAGGACATT 153
|||||
34  laSerIleGlyAspArgValThrIleThrCysArgAlaSerGlnGlyLe 50
|||||
154  AGGTATTATTAAATTTGGTATCAGCAGAAACAGGAAAAGCTCCTAAGCT 203
:::
51  AsnSerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLe 67
|||||
204  CCTGATCTATGTTCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTTCA 253
|||||
67  uLeuIleTyrValAlaSerThrLeuGlnSerGlyValProSerArgPheS 84
|||||
254  GCGCAGTGGATCTGGCAGAGATTCACCTCACCCTCAGCAGCGCTCGAG 303
|||||
84  erGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGln 100
|||||
304  CCTCAAGATTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCG 353
|||||
101  ProGluAspPheAlaSerTyrTyrCysGlnGlnPheAsnSerTyrProPh 117
|||||
354  GAGCTTCGGGCAAGGGACCAAGGTGGGAATCAAA 387
|||||
117  eThrPheGlyGlyGlyThrLysValGluIleArg 128

```

seq\_name: pir2:S52792

seq\_documentation\_block:

```

Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-May-1995 #sequence_revision 03-Aug-1995 #text_change 21-Jan-2000
C:Accession: S52792
R:Rocca, A.; Khamlichi, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Der
submitted to the EMBL Data Library, March 1995
A:Description: Light chain V region gene usage restriction and peculiarities in myelo
A:Reference number: S52789
A:Accession: S52792
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-129 <ROC>
A:Cross-references: EMBL:X85996; NID:g758598; PIDN:CAA59988.1; PID:g758599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

```

alignment\_scores:

```

Quality: 569.00 Length: 129
Ratio: 4.702 Gaps: 0
Percent Similarity: 93.798 Percent Identity: 85.271

```

alignment\_block:

US-09-019-441-3 x S52792 ..

Align seg 1/1 to: S52792 from: 1 to: 129

```

1  ATGCATGAGGTGCCCGCTCAGCTCCTGGGCTCCTCTGCTGCTGCTGCT 50
|||||
1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
|||||
51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
17  uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
|||||
101  CTGCATCTGTAGGGGACAGAGTCCACCTCAGCTTCAGGGCAAGTCAGGAC 150
|||||
34  erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
|||||
151  ATTAGGTATTATTAAATTTGGTATCAGCAGAAACAGGAAAAGCTCCTAA 200
|||||
51  IleAlaGlyTyrLeuAsnTrpTyrGlnGlnArgProGlyLysAlaProGl 67
|||||
201  GCTCCTGATCTATGTTCATCCAGTTTGCAAAGTGGGGTCCCATCAAGT 250
|||||

```

67 uLeuLeuIleTyrAlaAlaSerThrLeuArgSerGlyValProSerArgp 84  
251 TCAGCGCAGTGGATCTGGACAGATCTACTCTCACCCTGACAGCGCTG 300  
84 heSerGlySerGlySerGlyAlaAspPheThrLeuThrIleSerLeu 100  
301 CAGCCTGAAGATTTCGCGACTTATTACTGCTACAGGTTTATAGTACCCC 350  
101 GlnProGluAspSerAlaThrTyrTyrCysGlnGlnSerTyrGlyThrPr 117  
351 TCGGACGCTTCGGCCAGGCAAGGACCAAGTGGAAATCAAA 387  
117 oPheThrPheGlyProGlyThrLysValAspIleLys 129

seq\_name: pir2:S46372

seq\_documentation\_block:

Ig light chain variable region (VJ) - human

C:Species: Homo sapiens (man)

C:Date: 07-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: S46372

R:Bensimon, C.; Chastagner, P.; Zouali, M.

A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene re

A:Reference number: S46369; MUID:94313975

A:Accession: S46372

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-128 <BEN>

C:Cross-references: EMBL:227173

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

F:36-110/Domain: immunoglobulin homology <IMMS>

alignment\_scores:

Quality: 565.00 Length: 127

Ratio: 4.829 Gaps: 0

Percent Similarity: 92.126 Percent Identity: 86.614

alignment\_block:

US-09-019-441-3 x S46372 ..

Align seg 1/1 to: S46372 from: 1 to: 128

7 ATGAGGTCCCGCTCAGCTCTGGGCTCCTTCTGTCTGGTCCAGG 56  
1 MetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProG1 17  
57 TGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTCAT 106  
17 yAlaArgCysAlaIleArgIleThrGlnSerProSerSerLeuSerAla 34  
107 CTGTAGGGGACAGAGTCCACATCCTTGCAGGCAAGTCCAGGACATTAGG 156  
34 erThrGlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSer 50  
157 TATTATTAAATTGGTATCAGCAGAAACCCAGGAAAGCTCCTCAAGCTCT 206  
51 SerTyrLeuAlaThrTyrGlnGlnLysProGlyLysAlaProLysLeuLe 67  
207 GATCTATGTTCATCCAGTTCGAAAGTGGGGTCCCATCAAGTTTCAGCG 256  
67 uIleTyrAlaAlaSerThrLeuGlnSerGlyValProSerArgPheSerG 84  
257 GCAGTGTGATCTGGACAGATTCACCTCTCACCCTCAGCAGCTCCAGCCT 306  
84 lySerGlySerGlyThrAspPheThrIleSerCysLeuGlnSer 100  
307 GAAGATTTTCGAGCTTATTACTGCTACAGGTTTATAGTACCCCTCGGAC 356  
101 GluAspPheAlaThrTyrTyrCysGlnGlnTyrTyrSerTyrProArgTh 117

357 GTTCGCCCAAGGACCAAGGTGGAAATCAAA 387  
117 rPheGlyGlnGlyThrLysValGluIleLys 129  
seq\_name: pir2:S52789

seq\_documentation\_block:

Ig kappa chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 21-Jan-2000

C:Accession: S52789

R:Rocca, A.; Khamlich, A.A.; Touchard, G.; Mougnot, B.; Ronco, P.; Denoroy, L.; Der

submitted to the EMBL Data Library, March 1995

A:Description: Light chain V region gene usage restriction and peculiarities in myelo

A:Reference number: S52789

A:Accession: S52789

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-129 <ROC>

A:Cross-references: EMBL:X85995; NID:g758588; PID:CAA59987.1; PID:g758589

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:38-112/Domain: immunoglobulin homology <IMMS>

alignment\_scores:

Quality: 564.00 Length: 129

Ratio: 4.700 Gaps: 0

Percent Similarity: 93.023 Percent Identity: 84.496

alignment\_block:

US-09-019-441-3 x S52789 ..

Align seg 1/1 to: S52789 from: 1 to: 129

1 ATGACATGAGGTCCCGCTCAGCTCTGGGCTCCTTCTGTCTGGCT 50  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17  
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCTCTTCCCTGT 100  
17 uSerGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34  
101 CTCATCTGTAGGGACAGAGTCCACATCCTTGCAGGGCAAGTCAGGAC 150  
34 erAlaSerValGlyAspArgValThrIleThrCysGlnAlaSerGlnAsp 50  
151 ATTAGGTATTATTAAATTGGTATTCAGCAGAAACCCAGGAAAGCTCCTAA 200  
51 IleSerAsnTyrLeuAsnTrpTyrGlnLysProGlyLysAlaProLy 67  
201 GCTCCTGATCTATGTCATCCAGTTCGAAAGTGGGGTCCCATCAAGGT 250  
67 sLeuLeuIleHisAlaAlaSerSerLeuGluThrGlyValProSerArgp 84  
251 TCAGCGCAGTGGATCTGGGACAGATTCACCTCTCACCCTCAGCAGCGTG 300  
84 heSerGlySerGlySerGlyThrAspPheSerPheThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTTCGCGACTTATTACTGCTACAGGTTTATAGTACCCC 350  
101 GlnProGluAspLeuAlaThrTyrTyrCysGlnGlnTyrAspAsnLeuPr 117  
351 TCGGACGTTTCGGCCAGGACCAAGTGGAAATCAAA 387  
117 oLeuThrPheGlyGlyThrLysValGluIleLys 129

seq\_name: pir2:S40333

seq\_documentation\_block:

Ig kappa chain V-J region - human

C:Species: Homo sapiens (man)

C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40333  
 R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
 Eur. J. Immunol. 23, 3248-3271, 1993  
 A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
 A:Reference number: S40312; MUID:94080891  
 A:Accession: S40333  
 A>Status: preliminary; translation not shown  
 A:Molecule type: mRNA  
 A:Residues: 1-125 <KLE>  
 A:Cross-references: EMBL:X72443; NID:g441354; PIDN:CAA51111.1; PID:g441355  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:34-108/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
 Quality: 559.00 Length: 125  
 Ratio: 4.819 Gaps: 0  
 Percent Similarity: 92.800 Percent Identity: 87.200

alignment\_block:

US-09-019-441-3 x S40333 ..

Align seg 1/1 to: S40333 from: 1 to: 125

```

13 GTCCCCGCTCAGCTCCCTGGGCTCTTCTGCTGGCTCCAGGTGCAG 62
|||||
1 ValProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuProGlyAlaLy 17
:|||||
63 ATGTGCATCCAGATGACCCAGTCCATCTTCCTGCTGCTCATCTGTAG 112
|||||
17 sCysAspIleGlnMetThrGlnSerProSerThrLeuSerAlaSerValG 34
:|||||
113 GGGACAGAGTCACCATCTTCAGGGCAAGTCAGGACATTAGTATTAT 162
|||||
34 lyAspArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTrp 50
:|||||
163 TTAATTTGGTATCAGCAGAACACAGGAAGCTCCTAAGCTCCGATCTA 212
|||||
51 LeuAlaIrrpGlnGlnLysProGlyLysAlaProLysLeuLeuIleTy 67
|||||
213 TGTTCATCCAGTTTCAAGTGGGGTCCCATCAAGTTTCAGCGGCAGTG 262
|||||
67 rLysAlaSerSerLeuGluSerGlyValProSerArgPheSerGlySerG 84
|||||
263 GATCTGGCAGAGATTACCTCTCACCCTCAGCAGCCCTGCAGCCTGAAGAT 312
|||||
84 lySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProAspAsp 100
|||||
313 TTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGGTTCCG 362
|||||
101 PheAlaThrTyrrTyrrCysGlnGlnTyrrAsnSerTyrrProIrrpPheG 117
|||||
363 CCAAGGACCAAGTGGAATCAAA 387
|||||
117 yGlnGlyThrLysValGluIleLys 125

```

seq\_name: pir2:S24206

seq\_documentation\_block:

Ig kappa chain V region (Vx O12 and Vx O2) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 25-Feb-1994 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000  
 C:Accession: S24206; S24209  
 R:Pargent, W.; Meindl, A.; Thiebe, R.; Mitzel, S.; Zachau, H.G.  
 Eur. J. Immunol. 21, 1821-1827, 1991  
 A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated O region.  
 A:Reference number: S24205; MUID:91330953  
 A:Accession: S24206  
 A:Molecule type: DNA  
 A:Residues: 1-117 <PAR>  
 A:Cross-references: EMBL:X59315; NID:g33247; PIDN:CAA42002.1; PID:g33248  
 A:Experimental source: placenta

A:Genetics: G1  
 A:Accession: S24209  
 A:Molecule type: DNA  
 A:Residues: 1-117 <PAW>  
 A:Cross-references: EMBL:X59312; NID:g33252; PIDN:CAA41999.1; PID:g33253  
 A:Experimental source: placenta  
 A:Genetics: G2  
 C:Genetics: <G1>  
 A:Gene: Vx O12  
 A:Map position: 2  
 A:Introns: 19/1  
 C:Genetics: <G2>  
 A:Gene: Vx O2  
 A:Map position: 2  
 A:Introns: 19/1  
 C:Superfamily: immunoglobulin V region; immunoglobulin homology  
 C:Keywords: heterotetramer; immunoglobulin  
 F:38-112/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
 Quality: 557.00 Length: 117  
 Ratio: 4.973 Gaps: 0  
 Percent Similarity: 95.726 Percent Identity: 92.308

alignment\_block:

US-09-019-441-3 x S24206 ..

Align seg 1/1 to: S24206 from: 1 to: 117

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1 ATGCACATGAGGGTCCCGCTCAGCTCCTGGGCTCCTCTGCTCTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
:|||||
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCCCATCTTCCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
:|||||
101 CTGCATCTGTAGGGCAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
|||||
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACCAGGAAAGCTCTAA 200
|||||
51 lIleSerSerTyrrLeuAsnIrrpTyrrGlnGlnLysProGlyLysAlaProLy 67
|||||
201 GCTCCTCATCTATGTCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrrAlaAlaSerSerLeuGlnSerGlyValProSerArgP 84
|||||
251 TCAGCGCAGTGGATCTGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
|||||
301 CAGCCTCAAGATTTTCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrrTyrrCysGlnGlnSerTyrrSerThrPr 117

```

seq\_name: pir2:A49134

seq\_documentation\_block:

Ig kappa chain V-I region (ISE) - human (fragment)  
 C:Species: Homo sapiens (man)  
 C:Date: 19-Dec-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jan-2000  
 C:Accession: A49134; S25115  
 R:Rocca, A.; Khamilichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, C.  
 Clin. Exp. Immunol. 91, 506-509, 1993  
 A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in 11  
 A:Reference number: A49134; MUID:93185310





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1  ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGCTGGGT 50
|||||
1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
51  CCAGGTGCCAGATGTGACATCCAGATCACCCAGTCTCCATCTTCCCTGT 100
|||||
17  uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34
|||||
101 CTGCATCTGTAGGGACAGAGTCACCATCACTTGCAAGGCAAGTCAGGAC 150
|||||
34  erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
|||||
151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACAGGAAAGCTCCTAA 200
|||
51  IleSerArgTrpLeuAlaTrpTyrGlnGlnLysProGlyLysValProLy 67
|||||
201 GCTCTGATCATGTTCATCCAGTTTGCAAGTGGGTGCCCATCAAGGT 250
|||||
67  sLeuLeuIleTyrLysAlaSerSerLeuGluSerGlyValProSerArgp 84
|||||
251 TCAGCGGCAGTGGATCTGGGACAGAGTTCACCTCACCGTCAGCAGCCTG 300
|||||
84  heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
|||||
301 CAGCCTGAAGATTTGCCACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProAspAspPheAlaThrTyrTyrCysGlnGlnIntyrAsnSer.... 115
|||||
351 TCGGACGTTTCGGCCAAGGACCAAGGTGGAATCAAA 387
|||||
116 .TyrSerPheGlyProGlyThrLysValAspIleLys 127
```

OM of: US-09-019-441-3 to: SwissProt\_40:\* out\_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,  
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Command line parameters:

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-MODEL=frame+n2p.model -DEV=xlp  
-O=/cgn2_1/USPRO.spool/US09019441/runat_23092002_095259_6394/app_query.fasta_1.1860  
-DB=SwissProt_40 -OFMT=fastan -SUFFIX=rs -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -YGAPEXT=0.500  
-GAPOP=6.000 -GAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09019441.ecgnl_1.91 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPY -WAIT_THREADS=1
```

Search information block:

Query: US-09-019-441-3

Query length: 387

Database: SwissProt\_40:\*

Database sequences: 105224

Database length: 38719550

Search time (sec): 62.410000

score\_list:

Sequence	Strd Orig	ZScore	Escore	Len	Documentation
SwissProt_40:KV1W_HUMAN	+	578.00	1109.41	129	! P04431 homo sapiens (human)
SwissProt_40:KV1X_HUMAN	+	524.00	1005.33	129	! P04432 homo sapiens (human)
SwissProt_40:KV1J_HUMAN	+	521.00	1000.39	117	! P01602 homo sapiens (human)
SwissProt_40:KV1I_HUMAN	+	491.00	942.57	117	! P01601 homo sapiens (human)
SwissProt_40:KV1H_HUMAN	+	472.00	906.63	108	! P01600 homo sapiens (human)
SwissProt_40:KV1G_HUMAN	+	469.00	900.85	108	! P01599 homo sapiens (human)
SwissProt_40:KV1F_HUMAN	+	463.00	889.29	108	! P01610 homo sapiens (human)
SwissProt_40:KV5E_MOUSE	+	462.00	885.90	128	! P01637 mus musculus (mouse)
SwissProt_40:KV1E_HUMAN	+	456.00	875.80	108	! P01597 homo sapiens (human)
SwissProt_40:KV1S_HUMAN	+	456.00	875.80	108	! P01611 homo sapiens (human)
SwissProt_40:KV1B_HUMAN	+	452.00	868.09	108	! P01594 homo sapiens (human)
SwissProt_40:KV1O_HUMAN	+	452.00	868.09	108	! P01607 homo sapiens (human)
SwissProt_40:KV1N_HUMAN	+	450.00	864.23	108	! P01606 homo sapiens (human)
SwissProt_40:KV1F_HUMAN	+	449.00	862.30	108	! P01598 homo sapiens (human)
SwissProt_40:KV1J_HUMAN	+	448.00	860.38	108	! P01603 homo sapiens (human)
SwissProt_40:KV1A_HUMAN	+	447.00	858.45	108	! P01593 homo sapiens (human)
SwissProt_40:KV1L_HUMAN	+	444.50	852.10	129	! P18135 homo sapiens (human)
SwissProt_40:KV1P_HUMAN	+	444.00	852.67	108	! P01608 homo sapiens (human)
SwissProt_40:KV5G_MOUSE	+	444.00	851.07	130	! P01639 mus musculus (mouse)
SwissProt_40:KV1M_HUMAN	+	442.00	848.81	108	! P01605 homo sapiens (human)
SwissProt_40:KV1J_HUMAN	+	440.00	843.96	108	! P01609 homo sapiens (human)
SwissProt_40:KV1V_HUMAN	+	439.00	843.03	108	! P04430 homo sapiens (human)
SwissProt_40:KV1Y_HUMAN	+	439.00	843.03	108	! P80362 homo sapiens (human)
SwissProt_40:KV1C_HUMAN	+	434.00	833.39	108	! P01595 homo sapiens (human)
SwissProt_40:KV3M_HUMAN	+	433.50	830.90	129	! P18136 homo sapiens (human)
SwissProt_40:KV1D_HUMAN	+	431.50	828.65	107	! P01596 homo sapiens (human)
SwissProt_40:KV1L_HUMAN	+	430.00	825.68	108	! P01604 homo sapiens (human)
SwissProt_40:KV5H_MOUSE	+	428.00	821.14	117	! P01641 mus musculus (mouse)
SwissProt_40:KV1T_HUMAN	+	425.50	816.93	109	! P01612 homo sapiens (human)
SwissProt_40:KV4C_HUMAN	+	424.00	812.26	134	! P06314 homo sapiens (human)
SwissProt_40:KV5C_MOUSE	+	423.00	811.65	115	! P01635 mus musculus (mouse)
SwissProt_40:KV5F_MOUSE	+	423.00	811.65	115	! P01638 mus musculus (mouse)
SwissProt_40:KV3H_HUMAN	+	419.50	803.91	129	! P04207 homo sapiens (human)
SwissProt_40:KV5M_MOUSE	+	406.00	779.42	108	! P01646 mus musculus (mouse)
SwissProt_40:KV3K_HUMAN	+	404.00	774.11	128	! P06311 homo sapiens (human)
SwissProt_40:KV4B_HUMAN	+	402.50	770.89	133	! P06313 homo sapiens (human)
SwissProt_40:KV2F_HUMAN	+	400.50	767.03	133	! P06310 homo sapiens (human)
SwissProt_40:KV5K_MOUSE	+	399.00	765.93	108	! P01644 mus musculus (mouse)
SwissProt_40:KV5O_MOUSE	+	398.00	764.00	108	! P01648 mus musculus (mouse)
SwissProt_40:KV5N_MOUSE	+	397.00	762.08	108	! P01647 mus musculus (mouse)

SwissProt\_40:KV5J\_MOUSE + 395.00 758.22 1.4e-34 108 ! P01643 mus musculus (mouse)  
SwissProt\_40:KV5A\_HUMAN + 395.00 757.76 1.4e-34 114 ! P01625 homo sapiens (human)  
SwissProt\_40:KV5L\_MOUSE + 394.00 756.29 1.8e-34 108 ! P01645 mus musculus (mouse)  
SwissProt\_40:KV3I\_HUMAN + 394.00 755.75 1.8e-34 115 ! P04433 homo sapiens (human)  
SwissProt\_40:KV3J\_HUMAN + 392.50 752.79 2.7e-34 116 ! P04434 homo sapiens (human)

seq\_name: SwissProt\_40:KV1W\_HUMAN

seq\_documentation\_block:

ID KV1W\_HUMAN STANDARD; PRT; 129 AA.

AC P04431;

DT 13-AUG-1987 (Rel. 05, Created)

DT 13-AUG-1987 (Rel. 05, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Walker precursor.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85014148; PubMed=6091049;

RA Klobbeck H.G., Combriato G., Zachau H.G.;

RT "Immunoglobulin genes of the kappa light chain type from two human

FT lymphoid cell lines are closely related.";

RL Nucleic Acids Res. 12:6995-7006(1984).

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DR EMBL: X00965; CAA25477.1; ALT\_TERM.

DR PIR: A01883; K1HUWK.

DR HSP: P01607; 1REL.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR003596; Ig\_V.

DR Pfam: PF00047; Ig\_1.

DR SMART: SM00406; Igv\_1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 22

FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.

FT DOMAIN 23 45 FRAMEWORK-1.

FT DOMAIN 23 45 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 46 56 FRAMEWORK-2.

FT DOMAIN 57 71 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 72 78 FRAMEWORK-3.

FT DOMAIN 79 110 COMPLEMENTARITY-DETERMINING-3.

FT DOMAIN 111 119 FRAMEWORK-4.

FT DISULFID 45 110 BY SIMILARITY.

FT NON\_TER 129 129

SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

alignment\_scores:

Quality: 578.00 Length: 129

Ratio: 4.817 Gaps: 0

Percent Similarity: 93.023 Percent Identity: 88.372

alignment\_block:

US-09-019-441-3 x KV1W\_HUMAN ..

Align seg 1/1 to: KV1W\_HUMAN from: 1 to: 129

1 ATGCACATGAGGCTCCCGCTCAGCTCCTGGGCTCCTCTGCTGCTGCT 50

|||||

1 MetAspMetArgValProAlaGlnLeuLeuLeuLeuLeuLeu 17

|||||

51 CCCAGGTCACATGTCACATCCAGATGACCCAGCTCTCCATCTTCCCTGT 100

|||||

```

17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
101 CTGCATCTGTAGGGACAGAGTCACCATCCTGTCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
151 ATTAGTATTATTAAATGGGTATCAGCAGAAACACAGGAAAAGCTCTAA 200
|||||
51 IleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67
201 GCTCCTGATCTATGTGTCATCAGTTGCAAAAGTGGGTCCCATCAAGT 250
|||||
67 sleuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValThrSerArgp 84
251 TCAGGGCAGTGGATCTGGACAGAGTTCACCTCACCCTCAGCAGCCTG 300
|||||
84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCC 350
|||||
101 GlnProGluAspSerAlaThrTyrCysGlnGlnSerTyrSerThrIle 117
351 TCGGACGTTGGCCCAAGGACCAAGTGGAAATCAAA 387
|||||
117 uIleThrPheGlyGlnGlyThrArgLeuGluIleLys 129

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seq\_name: SwissProt\_40:KV1X\_HUMAN

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seq_documentation_block:
ID KV1X_HUMAN STANDARD; PRT; 129 AA.
AC P04432;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Ig kappa chain V-I region Daudi (update)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Klobbeck H.G.; Combratio G.; Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL Nucleic Acids Res. 12:6995-7006(1984).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X00966; CAA25478.1; ALT_TERM.
DR PIR; A01884; K1HUDI.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.
FT DOMAIN 23 45
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-4.
FT DISULFID 45 110 BY SIMILARITY.

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FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;

alignment_scores:
Quality: 524.00 Length: 129
Ratio: 4.517 Gaps: 0
Percent Similarity: 89.922 Percent Identity: 79.845

alignment_block:
US-09-019-441-3 x KV1X_HUMAN ..
Align seg 1/1 to: KV1X_HUMAN from: 1 to: 129

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1 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCTTCTGCTGTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTriple 17
51 CCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
17 uArgArgValArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
101 CTGCATCTGTAGGGACAGAGTCACCATCCTGTCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyHisAsn 50
151 ATTAGTATTATTAAATGGGTATCAGCAGAAACACAGGAAAAGCTCTAA 200
|||||
51 IleThrAsnPheLeuSerTrpTyrGlnGlnLysProGlyLysAlaProth 67
201 GCTCCTGATCTATGTGTCATCAGTTTGCAAAAGTGGGTCCCATCAAGT 250
|||||
67 rLeuLeuIleTyrAlaValSerAsnLeuGlnValGlyValProSerArgp 84
251 TCAGGGCAGTGGATCTGGACAGAGTTCACCTCACCCTCAGCAGCCTG 300
|||||
84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCC 350
|||||
101 GlnProGluAspPheAlaThrTyrCysGlnGlnAsnTyrAsnPheSe 117
351 TCGGACGTTGGCCCAAGGACCAAGTGGAAATCAAA 387
|||||
117 rPheThrPheGlyGlyThrLysValAspAsnLys 129

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seq\_name: SwissProt\_40:KV1J\_HUMAN

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seq_documentation_block:
ID KV1J_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK102 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L.; Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL Nature 288:730-733(1980).
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CC -----
DR EMBL; J00245; AAA59087.1; -
DR EMBL; Z00001; CAA77292.1; -
DR PIR; A01882; K1H012.
DR HSP; P01607; LREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 IG KAPPA CHAIN V-I REGION HK102.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 57 71 FRAMEWORK-2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 79 110 FRAMEWORK-3.
FT DOMAIN 111 >117 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12768 MW; AD1DF3A40AF1A49B CRC64;

alignment_scores:
  Quality: 521.00 Length: 115
  Ratio: 4.824 Gaps: 0
  Percent Similarity: 93.913 Percent Identity: 87.826

alignment_block:
US-09-019-441-3 x KVLJ_HUMAN
Align seg 1/1 to: KVLJ_HUMAN from: 1 to: 117

1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGCTCTGGCT 50
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGCTCCATCTCCCTGT 100
17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeu 34
101 CTGCATCTGTAGGGGACAGATGACCATCTGCGAGGCAAGTCAGGAC 150
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
151 ATTAGGTATTATTTAAATGGTATGATCAGCAAGAACCCAGGAAAGCTC 200
51 IleSerSerTrpLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCCTGATCTATGTCATCCAGTTCAGTTCGAAAGTGGGGTCCCAAGG 250
67 sLeuLeuIleTyrAspAlaSerSerLeuGluSerGlyValProSerArgp 84
251 TCAGCGCAGTGGATCTGGGACAGATTCACCTGTCACCGTCAGCAGCTG 300
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGCGACTTATTACTGTCTACAGGTTTATAGT 345
101 GlnProAspAspPheAlaThrTyrTyrCysGlnGlnTyrAsnSer 115

seq_name: SwissProt_40:KVLJ_HUMAN

seq_documentation_block:
ID KVLJ_HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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111
51 IIEserSerTriPLeuAlaTriPtyrGlnGlnLysProGluLysAlaProLy 67
201 GCTCTGATCTATGTGTCATCAGTTTGCAGAGTGGGTCCCATCAAGGT 250
67 sSerLeuIleTyAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGGAGTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGAGCCGCTG 300
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCTGAGAGTTTTCGACTTATTACTCTACAGGTTTATAGTACCC 350
101 GlnProGluAspPheAlaThrTyTyTyCysGlnGlnTyrAsnSerSerTyPr 117
351 T 351
117 O 117

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seq\_name: SwissProt\_40:KV1H\_HUMAN

seq\_documentation\_block:

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ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Hau.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=71032830; PubMed=4097974;
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein Hau); subdivision within
RT subgroups.";
RL Hoppe-Sevler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC PIR; A01868; KIHUHU.
DR HSSP; P80362; LWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;

```

alignment\_scores:

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Quality: 472.00 Length: 107
Ratio: 4.720 Gaps: 0
Percent Similarity: 93.458 Percent Identity: 85.047

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alignment\_block:

US-09-019-441-3 x KV1H\_HUMAN ..

Align seg 1/1 to: KV1H\_HUMAN from: 1 to: 108

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67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCGTCATCTGTAGGGGA 116
|||||

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```

1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValcIyAs 17
117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGACATAGGTATTATTAA 166
17 pArgValThrIleThrCysArgAlaSerGlnSerIleSerSerTyLeuS 34
167 ATTGTATATCAGCAGAACACAGGAAAGCTCTTAAGCTCCTGATCTATGTT 216
34 eTrpTyThrGlnGlnLysProGlyLysAlaProGlnValLeuIleTyAla 50
217 GCATCCAGTTTGCAGAGTGGGTCCCATCAAGTTTCAGGGCAGTGGATC 266
51 AlaSerSerLeuProSerGlyValProSerArgPheSerGlySerGlySe 67
267 TGGGACAGAGTCTACTCTCACCGTCAGAGCTGCAGCTGAAGATTG 316
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCCGCCAA 366
84 laThrTyTyTyCysGlnGlnAsnTyIleThrProThrSerPheGlyGln 100
367 GGGACCAAGGTGGAAATCAA 387
101 GlyThrArgValGluIleLys 107
seq_name: SwissProt_40:KV1G_HUMAN

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seq\_documentation\_block:

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ID KV1G_HUMAN STANDARD; PRT; 108 AA.
AC
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region GAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75059122; PubMed=4215718;
RA Laure C.J., Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal Igm-immunoglobulin
RT (macroglobulin Gal.), I. The amino acid sequence of the L-chain of
RT kappa-type, subgroup I.";
RL Hoppe-Sevler's Z. Physiol. Chem. 354:1503-1504(1973).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC PIR; A01867; KIHUGL.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11814 MW; CIAD3CB0F600FF73 CRC64;

```

alignment\_scores:

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Quality: 469.00 Length: 107
Ratio: 4.737 Gaps: 0
Percent Similarity: 92.523 Percent Identity: 86.916

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## alignment\_block:

US-09-019-441-3 x KVIG\_HUMAN

Align seg 1/1 to: KVIG\_HUMAN from: 1 to: 108

```
67 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGCTGCTAGGGGA 116
|||||
1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
|||||
117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||
17 pArgValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeu 34
|||||
167 ATTGGTATCAGCAGAAACAGGAAAGCTCTTAAGCTCCTGATCTATGTT 216
|||||
34 hrTrpTyrGlnGlnLysProGlyLysAlaProLysGluLeuIleTyrAla 50
|||||
217 GCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTTCAGCGGCAGTGGATC 266
|||||
51 AlaSerAsnLeuGlnSerGlyValProSerArgPheSerGlySerGlyAl 67
|||||
267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGAGCCTGAAGATTTTG 316
|||||
67 aGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
|||||
317 CGACTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTCCGGCAA 366
|||||
84 laThrTyrTyrCysLeuGlnGlnAsnSertYrProArgSerPheGlyGln 100
|||||
```

seq\_name: SwissProt\_40:KVIR\_HUMAN

## seq\_documentation\_block:

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ID KVIR_HUMAN STANDARD; PRT; 108 AA.
AC P01610;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region WEA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83273707; PubMed=6410398;
RA Goni F., Frangione B.;
RT "Amino acid sequence of the Fv region of a human monoclonal IgM
RT (protein WEA) with antibody activity against 3,4-pyruvylated
RT galactose in Klebsiella polysaccharides K30 and K33.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH
CC WALDENSTROM'S MACROGLOBULINEMIA.
DR PIR; A01876; KIHWE.
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR Immunoglobulin V region; Monoclonal antibody.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
```

FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11840 MW; 9249B61F0945618C CRC64;

## alignment\_scores:

Quality: 463.00 Length: 107  
Ratio: 4.773 Gaps: 0  
Percent Similarity: 90.654 Percent Identity: 85.981

## alignment\_block:

US-09-019-441-3 x KVIR\_HUMAN

Align seg 1/1 to: KVIR\_HUMAN from: 1 to: 108

```
67 GACATCCAGATGACCCAGTCTCCATCTTCCTGCTGCTGCTAGGGGA 116
|||||
1 AspileGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
|||||
117 CAGAGTCACCATCACTTGCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||
17 pArgValThrIleThrCysArgAlaSerGlnGlyIleArgAsnAspLeu 34
|||||
167 ATTGGTATCAGCAGAAACAGGAAAGCTCTTAAGCTCCTGATCTATGTT 216
|||||
34 hrTrpTyrGlnGlnLysProGlyThrAlaProLysArgLeuIleTyrGly 50
|||||
217 GCATCCAGTTTGCAGAGTGGGGTCCCATCAAGTTTCAGCGGCAGTGGATC 266
|||||
51 AlaThrSerLeuGlnSerGlyValProSerArgPheSerGlySerGly 67
|||||
267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCCTGAGCCTGAAGATTTTG 316
|||||
67 rGlyThrGluPheThrLeuThrIleAsnSerLeuGlnProGluAspPheA 84
|||||
317 CGACTTATTACTGTCTACAGTTTATAGTACCCTCGGACGTTCCGGCAA 366
|||||
84 laThrTyrTyrCysLeuGlnTyrSerSerPheProTyrThrPheGlyGln 100
|||||
367 GGGACCAAGTGGAAATCAA 387
|||||
101 GlyThrLysValGluValLys 107
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seq\_name: SwissProt\_40:KV5E\_MOUSE

## seq\_documentation\_block:

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ID KV5E_MOUSE STANDARD; PRT; 128 AA.
AC P01637;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-V region T1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81052342; PubMed=6776411;
RA Altenburger W., Steinmetz M., Zachau H.G.;
RT "Functional and non-functional joining in immunoglobulin light chain
RT genes of a mouse myeloma.";
RL Nature 287:603-607(1980).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00772; CAA24150.1;
DR PIR; A01920; KVMSTL.
```

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DR HSP; P01789; IMCP.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-V REGION TL.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 44 54 FRAMEWORK-2.
FT DOMAIN 55 69 FRAMEWORK-3.
FT DOMAIN 70 76 FRAMEWORK-4.
FT DOMAIN 109 117 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 128 128
SQ SEQUENCE 128 AA; 14385 MW; AFA5563D31BB7E05 CRC64;

alignment_scores:
  Quality: 462.00 Length: 127
  Ratio: 4.125 Gaps: 0
Percent Similarity: 88.189 Percent Identity: 66.929

alignment_block:
US-09-019-441-3 x KV5E_MOUSE

Align seg 1/1 to: KV5E_MOUSE from: 1 to: 128

7 ATGAGGTCCTCCGCTCAGCTCTGCTGGGCTCTCTGCTGCTGCTGCCAGG 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetArgThrProAlaGlnPheLeuGlyLeuLeuLeuLeuLeuLeuLeuLeu 17

57 TGCCAGATGTCACATCCAGATGACCCAGCTCTCCATCTTCCTGCTGCAT 106
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 yLeuLysCysAspLeuLysMetThrGlnSerProSerMetTyraLas 34

107 CTGTAGGCGACAGTCCACCTACTCTGTCAGGCAAGTCAGGACATTAGG 156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 erLeuGlyLysArgValThrLeuSerCysLysAlaSerGlnAspLeuA 50

157 TATTATTAAATGGTATCAGCAGAAACCCAGGAAAGCTCTTAAGCTCCT 206
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 SerTyrLeuThrThrPheGlnGlnLysProGlyLysSerProLysThrLe 67

207 GATCTATGTCATCCAGTTTGCAAGTGGGTCCTCCATCAAGGTTACGG 256
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 uLeuTyrArgAlaAsnArgLeuValAspGlyValProSerArgPheSerG 84

257 GCAGTGGATCTGGGACAGAGTTCATCTCAGCTCAGCAGCCTCAGCCT 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 lySerGlySerGlyGlnAspPheSerLeuThrLeuSerLeuLeuLys 100

307 GAAGATTTCGAGTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GluAspMetGlyLeuTyrCysLeuGlnLysGlnTyrAspGluPheProLeuTh 117

357 GTTCGGCCAGGACCAAGGTGGAAATCAA 387
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 rPheGlyAlaGlyThrLysLeuGluLeuLys 127

seq_name: SwissProt_40:KV1E_HUMAN

seq_documentation_block:
ID KV1E_HUMAN STANDARD; PRT; 108 AA.
AC P01597;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region DEE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=72053133; PubMed=5124396;
RA Milstein C.P.; Deverson E.V.;
RL "The amino acid sequence of a human kappa light chain.";
CC Blochem. J. 123:945-958(1971).
CR -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
DR PIR; A01865; KIHUDE.
DR HSP; P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 FRAMEWORK-4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11661 MW; BDD6E350017F1E51 CRC64;

alignment_scores:
  Quality: 456.00 Length: 106
  Ratio: 4.560 Gaps: 0
Percent Similarity: 94.340 Percent Identity: 80.189

alignment_block:
US-09-019-441-3 x KV1E_HUMAN

Align seg 1/1 to: KV1E_HUMAN from: 1 to: 108

67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCTGCTAGGGGA 116
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 ***Ile***MetThrGlnSerProSerLeuSerAlaSerValGlyAs 17

117 CAGAGTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 parValThrIleThrCysArgAlaGlyGlnSerValAsnLysTyrLeuA 34

167 ATTGGTATCAGCAGAAACCCAGGAAAGCTCTTAAGCTCCTCATCTATT 216
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysValLeuIlePheAla 50

217 GCATCCAGTTGCAAGTGGGTCCTCCATCAAGTTCAGCGCAGTGGATC 266
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 AlaSerLeuLysSerGlyValProSerArgPheSerGlySerGlySe 67

267 TGGGACAGATTCTACTCTCAGCTCAGCAGCCTCAGCCTCGGACGTTG 316
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 rGlyThrAspPheThrLeuThrIleSerGlyLeuLeuProGluAspPheA 84

317 CGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGACGTTGCGCAA 366
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 laThrTyrTyrCysGlnGlnSerTyrThrThrProTyrThrPheGlyPro 100

367 GGGACCAAGTGGAAATC 384
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GlyThrLysValGluMet 106

seq_name: SwissProt_40:KV1S_HUMAN

seq_documentation_block:
ID KV1S_HUMAN STANDARD; PRT; 108 AA.
AC P01611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
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DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region Wes.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=81092279; PubMed=6778806;  
 RP SEQUENCE.  
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;  
 RT "Preparative separation of the tryptic hydrolysate of a protein by  
 RT high-pressure liquid chromatography. The primary structure of a  
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein  
 RT Wes)."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR HSP; A01877; K1HUAU.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_V.  
 DR SMART; SM00406; Igv; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 25 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11608 MW; 782B14A649A60E45 CRC64;  
  
 alignment\_scores:  
 Quality: 456.00 Length: 107  
 Ratio: 4.606 Gaps: 0  
 Percent Similarity: 92.523 Percent Identity: 82.243  
  
 alignment\_block:  
 US-09-019-441-3 x KV1S\_HUMAN ..  
 Align seg 1/1 to: KV1S\_HUMAN from: 1 to: 108  
  
 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCATCTGTAGGGGA 116  
 1 AspIleGlnMetThrGlnSerProSerValSerAlaSerValGlyAs 17  
 117 CAGAGTCACCATCTACTGCGAGGCAAGTCAGGACATTAGGTATTATTAA 166  
 17 pArgValThrIleThrCysArgAlaSerGlnAspIleSerHisrLeuA 34  
 167 ATGGGTATCAGCAGAACACAGGAAAAGCTCCTAAGCTCTGATCTATGTT 216  
 34 laTrpTyrGlnGlnLysSerGlyLysAlaProLysLeuLeuIleTyrSer 50  
 217 GCAFTCCAGTTTGCAGAGTGGGGTCCCATCAAGGTTTCAGCGCGAGTGGATC 266  
 51 AlaSerSerLeuGluAenGlyValProSerArgPheSerGlySerGlySe 67  
 267 TGGACAGAGTTTCACTCTACCGTTCAGGCGTACGACGCTGCGAGCTTGGCAA 316  
 67 rGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84  
 317 CGACTTATTACTGTCTACAGGTTTATAGTACCCTCGGAGCTTCGGCCAA 366  
 84 laThrTyrPheCysGlnGlnAlaHisSerValProLeuThrPheGlyGly 100  
 367 GGGACCAAGGTGGAAATCAAA 387  
 101 GlyThrThrValAspIleLys 107

seq\_name: SwissProt\_40:KV1B\_HUMAN  
 seq\_documentation\_block:  
 ID KV1B\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01594;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region AU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein Au)."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72189444; PubMed=5028201;  
 RA Schiechl H., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones  
 RT protein Au)."  
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).  
 RN [2]  
 RP X-RAY CRYSTALLOGRAPHY.  
 RX MEDLINE=77022433; PubMed=1234024;  
 RA Fehlinhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,  
 RA Schwager P., Steigemann W., Schramm H.J.;  
 RT "The structure determination of the variable portion of the  
 RT Bence-Jones protein Au."  
 RL Biophys. Struct. Mech. 1:139-146(1975).  
 CC -!- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY  
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V  
 CC REGION OF THE KAPPA CHAIN REI.  
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR; A01862; K1HUAU.  
 DR HSP; P01607; 1REI.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR Pfam: PF00047; Ig\_V.  
 DR SMART; SM00406; Igv; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23 FRAMEWORK-1.  
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 35 49 FRAMEWORK-2.  
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 57 88 FRAMEWORK-3.  
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 98 107 FRAMEWORK-4.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11939 MW; E8011187EB6F6FB9 CRC64;

alignment\_scores:  
 Quality: 452.00 Length: 107  
 Ratio: 4.612 Gaps: 0  
 Percent Similarity: 91.589 Percent Identity: 83.178  
  
 alignment\_block:  
 US-09-019-441-3 x KV1B\_HUMAN ..  
 Align seg 1/1 to: KV1B\_HUMAN from: 1 to: 108  
  
 67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCATCTGTAGGGGA 116  
 1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17  
 117 CAGAGTCACCATCTACTGCGAGGCAAGTCAGGACATTAGGTATTATTAA 166  
 17 pArgValThrIleThrCysGlnAlaSerGlnAspIleSerAspTyrLeuA 34  
 167 ATGGGTATCAGCAGAACACAGGAAAAGCTCCTAAGCTCTGATCTATGTT 216

```
|||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrasp 50
|||||
217 GCATCCAGTTTCCAAAGTGGGTCCCAAGTTCACAGGTTTCAGCGCAGTGGATC 266
|||||
51 AlaSerAsnLeuGluSerGlyValProSerArgPheSerGlyGlySe 67
|||||
267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCTGCAGCGCTGAGAGATTG 316
|||||
67 rGlyAlaHisPheThrPheThrIleSerSerLeuGlnProGluAspIleA 84
|||||
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCCGCCAA 366
|||||
84 laThrTyrTyrCysGlnGlnTyrAspTyrLeuProTrpThrPheGlyGln 100
|||||
367 GGGACCAAGTGGAAATCAAA 387
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101 GlyThrLysValGluIleLys 107
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seq_name: SwissProt_40:KV10_HUMAN
seq_documentation_block:
ID KV10_HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Rel.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=76023758; PubMed=809329;
RA Faim W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rel.); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein REI refined at 2.0-A resolution."
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01873; KIHURE.
DR PDB; IREI; 17-FEB-84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
KW Immunoglobulin v region; Bence-Jones protein; 3d-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT STRAND 30 31
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FT STRAND 33 38
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alignment_scores:
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Ratio: 4.660 Gaps: 0
Percent Similarity: 91.509 Percent Identity: 82.075

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US-09-019-441-3 x KV10_HUMAN ..
Align seg 1/1 to: KV10_HUMAN from: 1 to: 108

67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCATCTGTAGGGGA 116
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
|||||
117 CAGAGTCACCATCACTTTCAGGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||
17 pArgValThrIleThrCysGlnAlaSerGlnAspIleIleLysTyrLeuA 34
|||||
167 ATTGCGTATCAGCAACACAGGAAAGCTCTTACAGCTCCATCATCTATT 216
|||||
34 snTrpTyrGlnGlnThrProGlyLysAlaProLysLeuLeuIleTyrGlu 50
|||||
217 GCATCCAGTTTGGAAAGTGGGTCCCATCAAGTTTCAGCGCAGTGGATC 266
|||||
51 AlaSerAsnLeuGlnAlaGlyValProSerArgPheSerGlySerGlySe 67
|||||
267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCTGCAGCGCTGAGAGATTG 316
|||||
67 rGlyThrAspTyrThrPheThrIleSerSerLeuGlnProGluAspIleA 84
|||||
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTCCGCCAA 366
|||||
84 laThrTyrTyrCysGlnGlnTyrGlnSerLeuProTyrThrPheGlyGln 100
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367 GGGACCAAGTGGAAATC 384
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101 GlyThrLysLeuGlnIle 106

seq_name: SwissProt_40:KV1N_HUMAN
seq_documentation_block:
ID KV1N_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
```

RT "Macroglobulin structure: variable sequence of light and heavy  
chains."; RT  
RL Science 169:56-59(1970).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
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CC PIR: A01872; KIHUOU.  
DR HSP: P01607; IREI.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00406; Igv: 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
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FT DOMAIN 98 107  
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SQ SEQUENCE 108 AA; 11777 MW; 8283D4A24105627E CRC64;

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US-09-019-441-3 x KVIF\_HUMAN ..

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67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTCCTGCTAGGGGA 116  
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1 AsplGlnMetThr\*\*\*SerProSerLeuSerAlaSerValGly\*\* 17  
CAGAGTCACCATCCTTGCAGGGCAAGTCCAGGACATTAGGTATTATTAA 166  
|||||  
17 \*ArgValThrIleThrCysArgAlaSer\*\*\*ThrIleSerSerTyrLeu\* 34  
167 ATTGGTATCAGCAGAACCCAGGAAAGCTCCTAGCTCCTGATCTATT 216  
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34 \*\*TrpTyr\*\*\*\*\*LysProGlyLysAlaPro\*\*\*LeuLeuIleTyrAla 50  
217 GCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTCAGCGCAGTGGATC 266  
|||||  
51 AlaSer\*\*\*LeuHisSerGlyValProSerArgPheSerGlySerGly 67  
267 TGGGACAGAGTTTCACTCTCAGCGTTCAGCAGCCTGACGCTGAAGATT 316  
|||||  
67 rGlyThr\*\*\*PheThrPheThrIleSerSerLeu\*\*\*Pro\*\*\*\*\*PheA 84  
317 CGACTTATTACTGCTACAGTTTATAGTACCCCTCGGAGCTTCGGCCAA 366  
|||||  
84 laThrTyrTyrCys\*\*\*\*\*SerTyrSerProThrThrPheGly\*\*\* 100  
367 GGGACCAAGGTGGAAATCAAA 387  
101 GlyThrArgLeu\*\*\*IleLys 107

seq\_name: SwissProt\_40:KVIF\_HUMAN

seq\_documentation\_block:

ID KVIF\_HUMAN STANDARD; PRT; 108 AA.

AC P01598;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region EU.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=71064023; PubMed=5489770;  
RA Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.; Amino  
RT "The covalent structure of a human gamma G-immunoglobulin. VI. Amino  
RL acid sequence of the light chain.";  
RL Biochemistry 9:3155-3161(1970).  
RN [2]  
RP DISULFIDE BOND.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Intrachain disulfide bonds.";  
RL Biochemistry 9:3188-3196(1970).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
DR PIR: A01866; KIHUOU.  
DR HSP: P01607; IREI.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00406; Igv: 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11788 MW; 9CD294F2F4D88823 CRC64;

alignment\_scores:

Quality: 449.00 Length: 107  
Ratio: 4.629 Gaps: 0  
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alignment\_block:

US-09-019-441-3 x KVIF\_HUMAN ..

Align seg 1/1 to: KVIF\_HUMAN from: 1 to: 108

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1 AsplGlnMetThrGlnSerProSerThrLeuSerAlaSerValGly 17  
117 CAGAGTCACCATCCTTGCAGGGCAAGTCCAGGACATTAGGTATTATTAA 166  
|||||  
17 \*ArgValThrIleThrCysArgAlaSerGlnSerIleAsnThrTrpLeuA 34  
167 ATTGGTATCAGCAGAACCCAGGAAAGCTCCTAGCTCCTGATCTATTG 216  
|||||  
34 laTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuMetTyrLys 50  
217 GCATCCAGTTTGCAAGTGGGTGCCATCAAGGTTTCAGCGCAGTGGATC 266  
|||||  
51 AlaSerLeuGluSerGlyValProSerArgPheIleGlySerGly 67  
267 TGGGACAGAGTTTCACTCTCAGCGTTCAGCAGCCTGACGCTGAAGATT 316  
|||||  
67 rGlyThrGluPheThrIleThrIleSerSerLeuGlnProAspPheA 84  
317 CGACTTATTACTGCTACAGTTTATAGTACCCCTCGGAGCTTCGGCCAA 366  
|||||  
84 laThrTyrTyrCysGlnGlnTyrAsnSerAspSerLysMetPheGlyGln 100  
367 GGGACCAAGGTGGAAATCAAA 387

|||||  
101 GlyThrLysValGluValLys 107  
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AC P01603;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-I region Ka.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76189985; PubMed=818073;  
RA Shinoda T.;  
RT "Comparative structural studies on the light chains of human  
RL J. Biochem. 77:1277-1296(1975).  
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01869; KIHUKA.  
DR HSSP; P80362; LWL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
DR Immunoglobulin V region; Bence-Jones protein.  
KW DOMAIN 1 23 FRAMEWORK-1.  
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 35 49 FRAMEWORK-2.  
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 57 88 FRAMEWORK-3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 98 107 FRAMEWORK-4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON\_TER 108 108  
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alignment\_scores:  
Quality: 448.00 Length: 107  
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alignment\_block:  
US-09-019-441-3 x KV1K\_HUMAN ..  
Align seg 1/1 to: KV1K\_HUMAN from: 1 to: 108

67 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGTCATCTGTAGGGGA 116  
|||||  
1 AspIleGlnMetThrGlnSerProSerThrLeuSerValSerValGlyAs 17  
117 CAGAGTCACCATCTCTGCAGGCGAGTCAGACATTAGGTATTTTAA 166  
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17 ParGValThrIleThrCysGluAlaSerGlnThrValLeuSerTyrLeuA 34  
167 ATTGGTATCATCAGCAAAACAGGAAAGCTCTAAGCTCTGATCTATGTT 216  
|||||  
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50  
217 GCATCCAGTTTGCAGAGTGGGGTCCCATCAAGGTTCCAGGCGCAGTGGATC 266  
|||||  
51 AlaSerSerLeuGluThrGlyValProSerArgPheSerGlyGlnGlySe 67  
267 TGGGACAGAGTTTCACTCTCACCCTCAGCAGCCTGCAGCCTGAAGATTTTG 316  
|||||  
67 rGlyThr\*\*\*PheThrPheThrIleSerSerVal\*\*\*Pro\*\*\*\*\*PheA 84

317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGACGTTTCGGCCAA 366  
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84 IaThrTyrCysGln\*\*\*TyrLeuAspLeuProArgThrPheGlyGln 100  
367 GGGACCAAGGTGGAATCAAA 387  
|||||  
101 GlyThrLysValAspLeuLys 107

OM of: US-09-019-441-3 to: SPTREMBL\_19:\* out\_format : pfs

Date: Sep 23, 2002 10:23 AM

About: Results were produced by the GenCore software, version 4.5.

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Command line parameters:

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Search information block:

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sp_human:Q9UL81	+	451.50	950.27	1.3e-44	107	! Q9UL81 homo sapiens (human). my
sp_human:Q9UL79	+	442.00	930.03	1.7e-43	108	! Q9UL79 homo sapiens (human). my
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sp_human:Q9UL86	+	343.50	721.05	7.5e-32	109	! Q9UL86 homo sapiens (human). my
sp_human:Q9UL74	+	335.00	703.92	7.4e-31	99	! Q9UL74 mus musculus (mouse). and
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sp_human:Q9UL12	+	316.50	656.63	1.3e-28	235	! Q9UL12 mus musculus (mouse). ar
sp_human:Q9UL78	+	315.00	661.32	1.7e-28	101	! Q9UL78 mus musculus (mouse). ar
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sp_mammal:Q9N0W5	+	301.00	630.92	7.8e-27	109	! Q9N0W5 oryctolagus cuniculus (r
sp_human:Q9UL76	+	298.00	625.65	1.7e-26	97	! Q9UL76 mus musculus (mouse). and
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sp_human:Q96E61	+	229.50	472.08	2.5e-18	236	! Q96E61 homo sapiens (human). ur
sp_human:Q925S1	+	226.00	465.40	6.5e-18	218	! Q925S1 mus musculus (mouse). ar
sp_human:Q96S80	+	214.50	447.56	1.3e-16	108	! Q96S80 homo sapiens (human). ar
sp_human:Q96JD1	+	202.50	421.77	3.4e-15	112	! Q96JD1 homo sapiens (human). ar
sp_human:Q99M11	+	201.50	412.74	5.2e-15	235	! Q99M11 mus musculus (mouse). hy
sp_human:Q96JD0	+	197.00	409.78	1.5e-14	116	! Q96JD0 homo sapiens (human). an

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sp\_human:Q9ET13 + 166.50 345.68 6.0e-11 109 ! Q9ET13 mus musculus (mouse).  
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ID Q9UL77 PRELIMINARY; PRT; 108 AA.  
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DT 01-MAY-2000 (TREMREL. 13, Created)  
DT 01-MAY-2000 (TREMREL. 13, Last sequence update)  
DT 01-DEC-2001 (TREMREL. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
(FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
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RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merve P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035037; AAD56273.1;  
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Ratio: 4.812 Gaps: 0  
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1 AspfGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17  
|||||  
117 CAGATCCACCATCACTTGCAGGGCAAGTCAGACATTAGGTATTATTAA 166  
|||||  
17 pAr9ValThrIleThrCysArgAlaSerGlnSerIleSerSerTyrLeuA 34  
|||||  
167 ATTGGTATCAGCAGAAACAGGAAAAGCTCTTAAGCTCCTGATCTATGTT 216  
|||||  
34 snTprTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla 50  
|||||  
217 GCATCCAGTTTGCRAAGTGGGGTCCCATCAAGGTTTCAGCGCAGTGGATC 266  
|||||  
51 AlaSerSerLeuGlnSerGlyValProSerSerArgPheSerGlySerGlyse 67  
|||||  
267 TGGGACAGAGTTCACTCTCAGCTCAGCAGCTGCAGCCTGAAGATTGTTG 316  
|||||  
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84  
|||||  
317 CGACTTATTACTGTCTACAGATTTTATAGTACCCCTCGACGCTCGGCCAA 366  
|||||  
84 laThrTyrTyrCysGlnGlnSerTyrSerThrSerThrPheGlyGlu 100  
|||||

```

367 GGGACCAAGGTGGAATCAAA 387
|||||
101 GlyThrLysValGluLeuLys 107

seq_name: sp_human:Q96SA9

seq_documentation_block:
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=97112075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

```

```

alignment_scores:
  Quality: 478.50      Length: 107
  Ratio: 4.785        Gaps: 1
Percent Similarity: 93.458 Percent Identity: 89.720

```

```
alignment_block:
US-09-019-441-3 x Q96SA9 ..
```

```
Align seg 1/1 to: Q96SA9 from: 1 to: 107
```

```

67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGGGA 116
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
117 CAGAGTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||
17 pArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTyrLeuA 34
167 ATTGGTATCAGCAGAAACCAGGAAAGCTCTAAGCTCTGATCTATGTT 216
|||||
34 snTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrAla 50
217 GCATCCAGTTTGCAGAGTGGGTCCTCAAGTTCAGCGCAGTGGATC 266
|||||
51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
267 TGGACACAGTTTCACTCTACCGTTCAGCAGCCTCCAGCTCAAGATTG 316
|||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPheA 84
317 CGACTTATTACTGCTACAGGTTTATAGTACCCCTCGGAGTTCGGCCAA 366
|||||
84 laThrTyrTyrCysGlnGlnSerTyrSerThr...LeuThrPheGlyGly 99
367 GGGACCAAGGTGGAATCAAA 387
|||||
100 GlyThrLysValGluLeuLys 106

```

```
seq_name: sp_human:Q9UL70
```

```
seq_documentation_block:
```

```

ID Q9UL70 PRELIMINARY; PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; -
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

```

```
alignment_scores:
```

```

  Quality: 455.00      Length: 107
  Ratio: 4.691        Gaps: 0
Percent Similarity: 90.654 Percent Identity: 83.178

```

```
alignment_block:
US-09-019-441-3 x Q9UL70 ..
```

```
Align seg 1/1 to: Q9UL70 from: 1 to: 108
```

```

67 GACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGCATCTGTAGGGGA 116
|||||
1 AspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
117 CAGAGTCACCATCACTTGCAGGCAAGTCAGGACATTAGGTATTATTAA 166
|||||
17 pArgValThrIleThrCysArgAlaSerGlnGlyIleSerSerTyrLeuA 34
167 ATTGGTATCAGCAGAAACCAGGAAAGCTCTAAGCTCTGATCTATGTT 216
|||||
34 laTrpTyrGlnGlnLysProGlyLysValProLysSerLeuIleTyrAla 50
217 GCATCCAGTTTGCAGAGTGGGTCCTCAAGTTCAGCGCAGTGGATC 266
|||||
51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
267 TGGACACAGTTTCACTCTACCGTTCAGCAGCCTCCAGCTCAAGATTG 316
|||||
67 rGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspValA 84
317 CGACTTATTACTGCTACAGGTTTATAGTACCCCTCGGAGTTCGGCCAA 366
|||||
84 laThrTyrTyrCysGlnLysTyrAsnSerAlaProArgThrPheGlyPro 100
367 GGGACCAAGGTGGAATCAAA 387
|||||
101 GlyThrLysLeuGluLeuLys 107

```

```
seq_name: sp_human:Q9UL81
```

```
seq_documentation_block:
```

```
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
```

```
AC Q9UL81;
```

DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035033; AAD56269.1; -;  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 FT NON\_TER 1  
 FT NON\_TER 107  
 SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

alignment\_scores:  
 Quality: 451.50 Length: 107  
 Ratio: 4.561 Gaps: 1  
 Percent Similarity: 92.523 Percent Identity: 84.112

alignment\_block:

US-09-019-441-3 x Q9UL81 ..

Align seg 1/1 to: Q9UL81 from: 1 to: 107

```

67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGA 116
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
1 AsplValMetThrGlnSerProSerSerLeuSerAlaSerValGlyAs 17
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
117 CAGAGTCACCATCACTTCAGGGCAAGTCCAGGACATTAGGTATTATTAA 166
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
17 parGValThrIleSerCysArgAlaSerGlnSerIleSerAsnTyrLeuA 34
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
167 ATTGGTATCAGCAGAAACAGGAAAGCTCTAAGCTCCTCATCTATGTT 216
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
34 snrTyrGlnGlnLysProGlyLysAlaProAsnLeuLeuIleTyrAla 50
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
217 GCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTCAGCGCAGTGGATC 266
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
51 AlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
267 TGGGACAGAGTTCACTCTCCGTCAGCAGCTGCAGCTGCAGCTGAGATTG 316
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
67 rGlyThrAspPheThrLeuThrIleSerGlyLeuGlnAlaGluAspPheA 84
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGTTTCGGCAA 366
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
84 laThrTyrTyrCysGlnGlnSerTyrSerAla...LeuThrPheGlyPro 99
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
367 GGGACCAAGGTGGAAATCAAA 387
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
100 GlyThrLysValAspIleArg 106

```

seq\_name: sp\_human:Q9UL79

seq\_documentation\_block:

ID Q9UL79 PRELIMINARY; PRT; 108 AA.  
 AC Q9UL79;  
 DT 01-MAY-2000 (TReMBLrel. 13, Created)  
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
 DE (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
 RT fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035035; AAD56271.1; -;  
 DR HSP; P01607; IREI.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 FT NON\_TER 1  
 FT NON\_TER 108  
 SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

alignment\_scores:  
 Quality: 442.00 Length: 107  
 Ratio: 4.702 Gaps: 0  
 Percent Similarity: 87.850 Percent Identity: 81.308

alignment\_block:

US-09-019-441-3 x Q9UL79 ..

Align seg 1/1 to: Q9UL79 from: 1 to: 108

```

67 GACATCCAGATGACCCAGTCTCCATCTCCCTGTCGTCATCTGTAGGGGA 116
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
1 AsplValMetThrGlnSerProSerLeuSerAlaSerThrGlyAs 17
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
117 CAGAGTCACCATCACTTCAGGGCAAGTCCAGGACATTAGGTATTATTAA 166
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
17 parGValThrIleSerCysArgMetSerGlnGlyIleSerSerTyrLeuA 34
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
167 ATTGGTATCAGCAGAAACAGGAAAGCTCTAAGCTCCTCATCTATGTT 216
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
34 laTyrTyrGlnGlnLysProGlyLysAlaProGluLeuLeuIleTyrAla 50
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
217 GCATCCAGTTTGCAAGTGGGGTCCCATCAAGGTTTCAGCGCAGTGGATC 266
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
51 AlaSerThrLeuGlnSerGlyValProSerArgPheSerGlySerGlySe 67
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
267 TGGGACAGAGTTCACTCTCCGTCAGCAGCTGCAGCTGCAGCTGAGATTG 316
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
67 rGlyThrAspPheThrLeuThrIleSerCysLeuGlnSerGluAspPheA 84
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGTTTCGGCAA 366
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
84 laThrTyrTyrCysGlnGlnTyrTyrSerPheProThrPheGlyGln 100
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
367 GGGACCAAGGTGGAAATCAAA 387
||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
101 GlyThrLysValGluIleLys 107

```

seq\_name: sp\_rodent:Q925S9

seq\_documentation\_block:

ID Q925S9 PRELIMINARY; PRT; 127 AA.  
 AC Q925S9;  
 DT 01-DEC-2001 (TReMBLrel. 19, Created)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
 DE IMMUNOGLOBULIN LIGHT CHAIN (FRAGMENT).

OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RA Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,  
RA Foon K.A., Chatterjee S.K.;  
RT "Construction and characterization of a chimeric fusion protein  
consisting of an anti-idiotypic antibody mimicking a breast cancer-  
associated antigen and the cytokine GM-CSF";  
RL Hybridoma 18:193-202(1999).  
DR EMBL; AF124721; AAK55120.1; -  
FT NON\_TER 127 127  
SQ SEQUENCE 127 AA; 13794 MW; 13F61BEBB981FA5 CRC64;

alignment\_scores:  
Quality: 439.00 Length: 127  
Ratio: 3.955 Gaps: 0  
Percent Similarity: 87.402 Percent Identity: 67.717  
alignment\_block:  
US-09-019-441-3 x Q925S9 ..  
Align seg 1/1 to: Q925S9 from: 1 to: 127

7 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCCTCTGCTCTGCTCCAGG 56  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 MetArgAlaProAlaGlnIleLeuGlyPheLeuLeuLeuLeuPheProG1 17  
57 TGCCAGATGTGACATCCAGTACCCAGTCTCCATCTCCCTGCTGCTGAT 106  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
17 yThrArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAla 34  
107 CTGTAGGGACAGTACCATCTCTGAGGCAAGTCCAGGACATAGG 156  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
34 erLeuGlyGlnArgValSerLeuThrCysArgAlaSerGlnAspIleGly 50  
157 TATTATTAAATTTGGTATCAGACAGAACCCAGGAAAGCTCTAGCTCT 206  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
51 IleAsnLeuHisTrpLeuGlnGlnGlnProAspGlyThrIleLysArgLe 67  
207 GATCTATGTTGCATCCAGTTTGCAGGTCCTCCATCAGGTTTCAGCG 256  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
67 uIleTyAlaThrSerSerLeuGlySerGlyValProLysArgPheSerG 84  
257 GCAGTGGATCTGGACAGAGTTCATCTCAGCGTCAGCAGCTCGAGCCT 306  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
84 lySerArgSerGlySerAspTySerLeuThrIleSerSerLeuGluSer 100  
307 GAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAC 356  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
101 GluAspPheValAlaTyTrpCysLeuGlnTyAlaSerSerProTyTrh 117  
357 GTTCGGCAAGGACCAAGTGGAAATCAAA 387  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
117 rPheGlyGlyGlyThrLysLeuGluIleLys 127

seq\_name: sp\_rodent:Q91WF8  
seq\_documentation\_block:  
ID Q91WF8 PRELIMINARY; PRT; 234 AA.  
AC Q91WF8;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 25.9 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC015292; AAH15292.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;

alignment\_scores:  
Quality: 435.00 Length: 127  
Ratio: 4.104 Gaps: 0  
Percent Similarity: 83.465 Percent Identity: 67.717  
alignment\_block:  
US-09-019-441-3 x Q91WF8 ..  
Align seg 1/1 to: Q91WF8 from: 1 to: 234

7 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCCTCTGCTCTGCTCCAGG 56  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 MetMetSerSerAlaGlnPheLeuGlyLeuLeuLeuLeuCysPheGlnG1 17  
57 TGCCAGATGTGACATCCAGTACCCAGTCTCCATCTCCCTGCTGCTGAT 106  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
17 yThrArgCysAspIleGlnMetThrGlnThrThrSerSerLeuSerAla 34  
107 CTGTAGGGACAGTACCATCTCTGAGGCAAGTCCAGGACATAGG 156  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
34 erLeuGlyAspArgValThrIleSerCysArgAlaSerGlnAspIleSer 50  
157 TATTATTAAATTTGGTATCAGACAGAACCCAGGAAAGCTCTAGCTCT 206  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
51 AsnTyLeuAsnTrpTyTrpGlnGlnLysProAspGlyThrValLysLeu 67  
207 GATCTATGTTGCATCCAGTTTGCAGGTCCTCCATCAGGTTTCAGCG 256  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
67 uIleTyTrpThrThrSerArgLeuTyLeuGlyValProSerArgPheSerG 84  
257 GCAGTGGATCTGGACAGAGTTCATCTCAGCGTCAGCAGCTCGAGCCT 306  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
84 lySerGlySerGlyThrAspTySerLeuThrIleSerAsnLeuGluGln 100  
307 GAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAC 356  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
101 GluAspIleAlaThrTyPheCysGlnGlnGlyAsnThrProProPheTh 117  
357 GTTCGGCAAGGACCAAGTGGAAATCAAA 387  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
117 rPheGlySerGlyThrLysLeuGluValLys 127

seq\_name: sp\_rodent:Q91WS9  
seq\_documentation\_block:  
ID Q91WS9 PRELIMINARY; PRT; 233 AA.  
AC Q91WS9;  
DT 01-DEC-2001 (TReMBLrel. 19, Created)  
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 25.8 KDA PROTEIN (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC013496; AAH13496.1; -  
KW Hypothetical protein.





Align seg 1/1 to: Q920B6 from: 1 to: 109

```
67 GACATCCAGATGACCCAGTCTCCATCTCCCTGCTGTCATCTGTAGGGCA 116
|||||
1 AspIleGlnMetThrGlnSerProAlaSerLeuSerAlaSerValGlyGI 17
|||||
117 CAGAGTCACCATCTACTGTCAGGGCAGTCCAGGACATAGTATTATTAA 166
|||||
17 ThrValThrIleThrCysArgAlaSerGlyAsnIleHisAsnTyrLeuA 34
|||||
167 ATTGTATCAGCAGAACACCAAGTCCCTAAGCTCTGCTGATCTATGTT 216
|||||
34 lAtPrpYrGlnGlnLysGlnGlyLysSerProGlnLeuLeuValTyrAsn 50
|||||
217 GCATCCAGTGTTCACAAAGTGGGTCCCATCAAGTTCAGCGGCAGTGGATC 266
|||||
51 AlaLysThrLeuAlaAspGlyValProSerArgPheSerGlySerGlyse 67
|||||
267 TGGGACAGATTCACCTCTACCGTCCAGCAGCGCTGACGCTCAAGATTTTG 316
|||||
67 rGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnProGluAspPheG 84
|||||
317 CGACTTATTACTGCTACAGGTTTATAGTACCCCTCGGACGCTCGGCCAA 366
|||||
84 lYSerTyrTyrCysGlnHisPheTrpSerThrProTrpThrPheGlyGly 100
|||||
367 GGGACCAAGTGGAAATCAAA 387
|||||
101 GlyThrLysLeuGluLeuLys 107
```

seq\_name: sp\_rodent:Q9QYF0

```
seq_documentation_block:
ID Q9QYF0 PRELIMINARY; PRT; 298 AA.
AC Q9QYF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse)
GN CN 8.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=SPLEEN;
RX MEDLINE=20183931; PubMed=10706631;
RA Shinohara N., Demura T., Fukuda H.;
RT "Isolation of a vascular cell wall-specific monoclonal antibody
recognizing a cell polarity by using a phage display subtraction
method."
RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000).
DR EMBL; AB036341; BAA88633.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 2.
SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;
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alignment\_scores:  
Quality: 392.00 Length: 111  
Ratio: 4.041 Gaps: 0  
Percent Similarity: 87.387 Percent Identity: 65.766

alignment\_block:

US-09-019-441-3 x Q9QYF0 ..

Align seg 1/1 to: Q9QYF0 from: 1 to: 298

```
55 GGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGTC 104
|||||
```

```
169 GlyGlyGlySerAspIleGlnLeuThrGlnSerProAlaSerLeuSerAl 185
|||||
105 ATCTGTAGGGCAGAGTCCATCTGAGGGCAAGTCCAGGACATTA 154
|||||
185 aserValGlyGluThrValThrIleThrCysArgAlaSerGlyAsnIleH 202
|||||
155 GGTATTATTAAATTTGGTATCAGCAGAACCAAGGAAAAGCTCTTAAGCTC 204
|||||
202 lAsnTyrLeuAlaTrpTyrGlnGlnLysGlnGlyLysSerProGlnLeu 218
|||||
205 CTGATCTATGTTGATCCAGTTCGAAAGTGGGTCCCATCAAGTTCAG 254
|||||
219 LeuValTyrAsnAlaLysThrLeuAlaAspGlyValProSerArgPheS 235
|||||
255 CGCGAGTGGATCTGGGACAGATTCACCTCTCACCGTCCAGCAGCTCCAGC 304
|||||
235 rGlySerGlySerGlyThrGlnTyrSerLeuLysIleAsnSerLeuGlnP 252
|||||
305 CTGAAGATTTTGGGACTTACTCTCTACAGGTTTATAGTACCCCTCGG 354
|||||
252 roGluAspPheGlySerTyrTyrCysGlnHisPheTrpThrProTyr 268
|||||
355 ACGTTTCGGCCCAAGGACCAAGTGGAAATCAAA 387
|||||
269 ThrPheGlyGlyGlyThrLysLeuGluLeuLys 279
```

seq\_name: sp\_rodent:Q9RIA5

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seq_documentation_block:
ID Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
antibody (Mab 7, its light and heavy chains) and construction of a
single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE95E2A CRC64;
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alignment\_scores:  
Quality: 385.00 Length: 107  
Ratio: 4.096 Gaps: 0  
Percent Similarity: 87.850 Percent Identity: 68.224

alignment\_block:

US-09-019-441-3 x Q9RIA5 ..

Align seg 1/1 to: Q9RIA5 from: 1 to: 214

```
67 GACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGTCATCTGTAGGGGA 116
|||||
```

```

1  AspileGlnLeuThrGlnSerProSerSerMetTyrAlaSerLeuGlyG1 17
117 CAGAGTACCACCTGTCAGGGCAAGTCAGGACATTAGTATTATTAA 166
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17  uArgValThrIleThrCysLysAlaSerGlnAspIleAsnSerTyrLeuS 34
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
167 ATTGGTATCAGCAGAAACACGAAAGCTCCTAAGCTCCTGATCTATGTT 216
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34  erTrpPheGlnGlnLysProGlySerProLysThrLeuIleTyrArg 50
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
217 GCATCCAGTTTGAAGAGTGGGGTCCCATCATCAAGTTTCAGCGGAGTGATC 266
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  AlaAsnArgLeuValAspGlyValProSerArgPheSerGlySerGlySe 67
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
267 TGGGACAGAGTTCCTACTCCAGCTCAGCAGCCGTCAGCCGTCGAAGTTTG 316
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67  rGlyGlnAspTyrSerLeuThrIleSerSerLeuGluTyrGluAspMetG 84
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
317 CGACTTATTACTGTCTACAGGTTTATAGTACCCCTCGGAGCTTCGGCCAA 366
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84  lYleIleTyrCysLeuGluTyrAspGluPheProPheThrPheGlySer 100
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
367 GGGACCAAGGTGGAATCAAA 387
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 GlyThrLysLeuGluIleLys 107

```

seq\_name: sp\_rodent:Q99M37

```

seq_documentation_block:
ID Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 26.3 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020335; AA02035.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

```

```

alignment_scores:
  Quality: 371.00      Length: 132
  Ratio: 3.404        Gaps: 2
Percent Similarity: 82.576 Percent Identity: 53.788

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alignment\_block:

US-09-019-441-3 x Q99M37 ..

Align seg 1/1 to: Q99M37 from: 1 to: 238

7 ATGAGGTCCTCCGCTCAGCTCTGGGCTCCTTCTGTCTGGCTCCAGG 56

```

|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  MetLysLeuProValArgLeuLeu...ValLeuMetPheTrpIleProAl 16
57  TGCACGATGTGCATCATGACATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
16  aSerSerSerAspValValMetThrGlnThrProLeuSerLeuProValS 33
107 CTCTAGGGGACAGAGTCACCATCCTTTCAGGCAAGTCAGGACATTAGG 156
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
33  erLeuGlyAspGlnAlaSerIleSerCysArgSerSerGlnSerIleVal 49
157 TAT .....TATTTAAATTTGGTATCAGCAGAAACACGAGAA 191
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
50  HisSerAsnGlyAsnThrTyrLeuGluTrpTyrLeuGlnLysProGlyG1 66
192 AGTCTCTAAGCTCTCTGATCTATGTTGCATCCAGTTTGTTCGAAAGTGGGTC 241
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
66  nSerProLysLeuLeuIleTyrLysValSerAsnArgPheSerGlyValP 83
242 CATCAGGTTTCAGGCGAGTGGATCTGGGACAGAGTTCACCTCTCACCGTC 291
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83  roAspArgPheSerGlySerGlySerGlyThrAspPheThrLeuLysIle 99
292 AGCAGCTGCAGCTGAAGATTTTGCACCTTATTACTGTCTACAGGTTTA 341
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
100 SerArgValGluAlaGluAspLeuGlyValTyrTyrCysPheGlnGlySe 116
342 TAGTACCCCTCGGAGCTTCGGCCAAAGGACCAAGTGGGAATCAAA 387
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 rHisValProTyrThrPheGlySerGlyThrLysLeuGluIleLys 131

```

seq\_name: sp\_human:Q9UL83

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seq_documentation_block:
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-WAY-2000 (TReMBLrel. 13, Created)
DT 01-WAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA968EA CRC64;

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alignment_scores:
  Quality: 368.00      Length: 107
  Ratio: 4.044        Gaps: 0
Percent Similarity: 85.047 Percent Identity: 65.421

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alignment\_block:

US-09-019-441-3 x Q9UL83 ..

Align seg 1/1 to: Q9UL83 from: 1 to: 108

67 GACATCCAGATGACCCAGCTCCATCTCCCTGCTGTCATCTGCTAGGGGA 116  
1 GluileValMetThrGlnSerProAlaThrLeuSerValSerProGlycyl 17  
117 CAGGTCCTACCATCTGCTGAGGCGAAGTCAGGACATTTAGGTATTATTAA 166  
17 uAgaLathrLeuSerCysArgAlaSerGlnSerValSerSerAsnLeuA 34  
167 ATTGTATCAGAGAAACAGAGAAAGCTCTAAGCTCTGATCTATGTTT 216  
34 laTrpTyrGlnGlnLysProGlyGlnAlaProArgLeuLeuIleTyrCys 50  
217 GCATCCAGTTTCCAAAGTGGGTCCTCCATCAGGTCACGGCAGTGGATC 266  
51 AlaSerThrArgAlaThrGlyIleProAlaArgPheSerGlySerGlyse 67  
267 TGGGACAGAGTTCACTCTCACCGTCAGCAGCTGCAGCTCGAAGATTGTG 316  
67 rGlyThrGluPheThrLeuThrIleSerSerLeuGlnPheGluAspPheA 84  
317 CGACTTATTACTGTACAGGTTTATAGTACCCCTCGGACGTTGCGCCAA 366  
84 laValTyrTyrCysGlnHisTyrAsnAsnTrpProPheThrPheGlyPro 100  
367 GGGACCAAGTGGAAATCAAA 387  
101 GlyThrLysValAspIleLys 107

seq\_name: sp\_rodent:Q91XL0

seq\_documentation\_block:  
ID Q91XL0 PRELIMINARY; PRT; 211 AA.  
AC Q91XL0;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DE ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,  
DE CLONE:0610010P20, FULL INSERT SEQUENCE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,  
RA Arakawa T., Carninci P., Fukuda S., Hiramoto K., Hiraoka T., Hori F.,  
RA Hanagaki T., Hara A., Hayatsu N., Izawa M., Kato H., Kawai J., Kojima Y.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,  
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,  
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,  
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,  
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,  
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,  
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=21085660; PubMed=11217851;  
RA RIKEN FANTOM Consortium;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=99279253; PubMed=10349636;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Meth. Enzymol. 303:19-44(1999).  
RN [4]

RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=20499374; PubMed=11042159;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
RL Prepare full-length cDNA libraries for rapid discovery of new genes.";  
RN Genome Res. 10:1617-1630(2000).  
[5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;  
RX MEDLINE=20530913; PubMed=11076861;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
RL sequencing pipeline with 384 multicapillary sequencer.";  
RN Genome Res. 10:1757-1771(2000).  
DR EMBL: AK002514; BAB22154.1;  
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8BA50163 CRC64;

alignment\_scores:

Quality: 367.00 Length: 104  
Ratio: 3.989 Gaps: 0  
Percent Similarity: 88.462 Percent Identity: 65.385

alignment\_block:

US-09-019-441-3 x Q91XL0 ..

Align seg 1/1 to: Q91XL0 from: 1 to: 211

76 ATGACCAGCTCCATCTCCCTGCTGTCATCTGCTAGGGGACAGAGTCAC 125  
1 MetThrGlnSerProAlaSerLeuSerValSerValGlyGluThrValTh 17  
126 CATCCTTGCAGGCAAGTCAGGACATTAGGTATTATTAAATGGTATC 175  
17 rIleThrCysArgAlaSerGluAsnIleTyrSerAsnLeuAlaTrpTyrG 34  
176 AGCAGAAACCCAGGAAAGCTCTAAGCTCTGATCTATGTTGCATCCAGT 225  
34 InGlnLysGlnGlyLysSerProGlnLeuLeuValTyrAlaAlaThrAsn 50  
226 TTGCAAAAGTGGGTCCCATCAAGTTCAGGGCAGTGGATCTGGGACAGA 275  
51 LeuAlaAspGlyValProSerArgPheSerGlySerGlyThrG 67  
276 GTTCACCTCTCCAGCTCAGCAGCTCGACCTCGAAGATTTTCGAGCTATT 325  
67 nTyrSerLeuLysIleAsnSerLeuGlnSerGluAspPheGlySerTyrP 84  
326 ACTGCTCTACAGTTTATAGTACCCCTCGGACGTTTCGCCAAGGGACCAAG 375  
84 heCysGlnHisPheTrpGlyThrProArgThrPheGlyGlyThrLys 100  
376 GTGGAATCAAA 387  
101 LeuGluIleLys 104

OM of: US-09-019-441-3 to: Pending\_Patents\_AA\_New:\* out\_format : pfs

Date: Sep 23, 2002 9:59 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

-MODEL=frame+ntp.model -DEV=xlpl  
-O=/cgn2\_1/USP01/spool/US09019441/runat\_23092002\_095258\_6341/app\_query.fasta\_1.1860  
-DB=Pending\_Patents\_AA\_New -QFMT=fastan -SUFFIX=rapn  
-GAPOP=12.000 -GAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000  
-LGAPEXT=0.000 -FGAPOP=4.500 -OGAPEXT=0.050 -XGAPOP=10.000  
-XGAPEXT=0.500 -FGAPOP=6.000 -FGAPEXT=7.000 -XGAPOP=10.000  
-LGAPEXT=0.500 -DELOP=6.000 -DELEXT=7.000 -START=1  
-MATRIX=blosom62 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200  
-THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pfs -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US09019441 @CGN1\_1.60 -NCPU=6 -ICPU=3 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -NO\_XLPXY -WAIT -THREADS=1

Search information block:

Query: US-09-019-441-3

Query length: 387

Database: Pending Patents\_AA\_New.\*

Database sequences: 949130

Database length: 267991220

Search time (sec): 353.570000

score.list:

Sequence	Strd Orig	zScore	EScore	Len	Documentation
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107543 +			600.50	1024.50	1.1e-48
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-10-206-008-639 +			595.00	1012.19	3.7e-48
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-10 +			594.50	1010.14	4.2e-48
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107484 +			592.00	1010.52	7.0e-48
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-1 +			590.50	1003.30	1.0e-47
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-181820 +			588.00	1004.06	1.7e-47
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-132274 +			586.00	1001.04	2.6e-47
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-12275 +			586.00	1000.64	2.6e-47
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-65658 +			581.00	991.97	7.7e-47
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71040 +			578.50	983.80	1.4e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71830 +			578.00	987.11	1.5e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-56448 +			578.00	987.04	1.5e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-107469 +			578.00	986.91	1.5e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-89619 +			577.00	985.53	1.9e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-13229 +			576.00	983.50	2.3e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-831-805A-13 +			573.50	974.26	4.2e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-106755 +			573.00	978.43	4.5e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-93259 +			571.00	974.83	6.9e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-13277 +			571.00	974.83	6.9e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-55913 +			570.00	974.77	6.9e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-14709 +			570.00	973.25	8.6e-46
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-81806 +			569.00	971.60	1.1e-45
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-10-206-008-852 +			568.00	964.46	1.4e-45
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-81852 +			565.00	964.83	2.6e-45
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-81805 +			564.00	963.06	3.2e-45
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-10-006-593-69 +			562.00	954.85	5.2e-45
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/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-118978 +			556.00	940.40	1.9e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-139930 +			555.50	944.51	2.1e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-34437 +			554.00	945.24	2.9e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-71822 +			553.00	944.14	3.6e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-48050 +			550.00	934.15	7.1e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-85831 +			549.00	937.37	8.6e-44
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-84560 +			548.00	935.86	1.1e-43
/cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-15225 +			548.00	935.66	1.1e-43
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/cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-85805 + 546.00 932.25 1.7e-4  
/cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-71308 + 545.00 930.99 2.1e-4  
/cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-123222 + 544.00 928.96 2.6e-4  
/cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-71144 + 543.00 927.99 3.2e-4  
/cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-43135 + 542.50 926.79 3.6e-4

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-120343

seq\_documentation\_block:

; Sequence 120343, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 120343  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-120343

alignment\_scores:

Quality: 610.00 Length: 129  
Ratio: 4.959 Gaps: 0  
Percent Similarity: 95.349 Percent Identity: 92.248

alignment\_block:

US-09-019-441-3 x US-09-791-537-120343 ..

Align seg 1/1 to: US-09-791-537-120343 from: 1 to: 143

1 ATGCACATGAGGTCCTCCCGCTCAGCTCCTGGGGCTCTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17  
|||||  
51 CCCAGGTGCCAGATGTACATCCAGATGACCCAGTCTCCATCTCCCTGT 100  
|||||  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34  
|||||  
101 CTGCATCTGTAGGGACAGATCACCATCCTTGCAGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50  
|||||  
151 ATTAGGTATTATTAAATTGTTGATCATCAGAGAACACAGGAAAGCTCTAA 200  
|||||  
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
|||||  
201 GCTCCTCATCTATCTTCATCCAGTTCGAAAGTGGGGTCCCATCAAGGT 250  
|||||  
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84  
|||||  
251 TCAGCGCAGTGGATCTGGGACACAGTTCCTCTCACCGTCAGCAGCTG 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
|||||  
301 CAGCCTGAAGATTTTGGCAGCTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117  
|||||  
351 TCGGACGTTTCGGCCCAAGGACCAAGTGGGAATCAAA 387  
|||||  
117 otrPThrPheGlyGlnGlyThrLysValGluIleLys 129

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-107543

seq\_documentation\_block:

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; Sequence 107543, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107543
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-107543

alignment_scores:
    Quality: 600.50      Length: 130
    Ratio: 4.882         Gaps: 1
    Percent Similarity: 94.615    Percent Identity: 91.538

alignment_block:
US-09-019-441-3 x US-09-791-537-107543 ..

Align seg 1/1 to: US-09-791-537-107543 from: 1 to: 144

1  ATGCATATGAGGGTCCCGCTCAGCTCTCTGGGCTCTCTGCTCTGCT 50
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1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

51  CCCAGGTGCCAGATGTGACATCCAGATCCAGATCCAGATCCAGATCCAGT 100
|||||
17  uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34

101 CTGCATCTGTAGGGAGCAGAGTCACTTCAGGCGCAAGTCAGGAC 150
|||||
34  erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTAATTTGGTATTCAGCAGAAACAGGAAAGTCCTAA 200
|||||
51  IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67

201 GCTCCTCATCTATCTTCATCCAGTTTGCAGAGTGGGTCCTCATCAAGT 250
|||||
67  sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84

251 TCAGCGGCAGTGGATCTGGACAGAGTTCACCTCAGCGTCAGCAGCCTG 300
|||||
84  heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCCTGAAGATTTCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117

351 TCGG...ACGTCGGCAAGGACCAAGTGGAAATCAAA 387
|||||
117  oProTrpThrPheGlyGlnGlyThrLysValGluIleLys 130

seq_name: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:US-10-206-008-639

seq_documentation_block:
; Sequence 639, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT53CLN
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/228,924
; PRIOR FILING DATE: 2000-08-30
; PRIOR APPLICATION NUMBER: 60/224,518
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,369
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/224,519
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,964
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/241,809
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/249,299
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/236,327
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/241,785
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/244,617
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 60/225,268
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/236,368
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/251,856
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/251,868
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/229,344
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/234,997
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: 60/229,343
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
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;	PRIOR APPLICATION NUMBER: 60/249,211	;
;	PRIOR FILING DATE: 2000-11-17	;
;	PRIOR APPLICATION NUMBER: 60/249,215	;
;	PRIOR FILING DATE: 2000-11-17	;
;	PRIOR APPLICATION NUMBER: 60/249,264	;
;	PRIOR FILING DATE: 2000-11-17	;
;	PRIOR APPLICATION NUMBER: 60/249,214	;
;	PRIOR FILING DATE: 2000-11-17	;
;	PRIOR APPLICATION NUMBER: 60/249,297	;
;	PRIOR FILING DATE: 2000-11-17	;
;	PRIOR APPLICATION NUMBER: 60/232,400	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/231,242	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/232,081	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/232,080	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/231,414	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/231,244	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/233,054	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/233,063	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/232,397	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/232,399	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/232,401	;
;	PRIOR FILING DATE: 2000-09-14	;
;	PRIOR APPLICATION NUMBER: 60/241,808	;
;	PRIOR FILING DATE: 2000-10-20	;
;	PRIOR APPLICATION NUMBER: 60/241,826	;
;	PRIOR FILING DATE: 2000-10-20	;
;	PRIOR APPLICATION NUMBER: 60/241,786	;
;	PRIOR FILING DATE: 2000-10-20	;
;	PRIOR APPLICATION NUMBER: 60/241,221	;
;	PRIOR FILING DATE: 2000-10-20	;
;	PRIOR APPLICATION NUMBER: 60/246,475	;
;	PRIOR FILING DATE: 2000-11-08	;
;	PRIOR APPLICATION NUMBER: 60/231,243	;
;	PRIOR FILING DATE: 2000-09-08	;
;	PRIOR APPLICATION NUMBER: 60/233,055	;

alignment block:

Align seg 1/1 to: US-10-206-008-639 from: 1 to: 205

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6  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriple 22
   |||||
   |||||
   |||||
   |||||
   |||||
51 CCCAGGTGCCAGATGTCACATCCAGATGACCCAGTCTCCATCTTCCCTGCT 100
   |||||
   |||||
   |||||
   |||||
   |||||
22  uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 39
   |||||
   |||||
   |||||
   |||||
   |||||
101 CTGCATCTCTTAGGGGACAGAGTCACCATCTGTCAGGCGCAAGTCAGGAC 150
   |||||
   |||||
   |||||
   |||||
   |||||
39  erAlaserValGlyAspArgValThrIleThrCysArgAlaSerGlnIle 55
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   |||||
151 ATTAGGTATTATTAAATTCGTATCAGCAGAAACGAGGAAAGCTCCTTAA 200
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   |||||
   |||||
   |||||
   |||||
56  IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 72
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   |||||
   |||||
201 GCTCCTCGATCTATGTTCATCTCCAGTCTTGCAAGGTGGGTCCCATCAAGGT 250
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1:::|||||
72 spheLeuIleTyrGlyAlaSerSerLeuGlnSerGlyValProSerArgp 89
251 TCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
89 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 105
301 CAGCCTGAAGATTTCGCACTATTACTGTCTACAGGTTTATAGTACCCC 350
106 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrThrPr 122
351 TCGGACGTTTCGCCCAAGGACCAAGTGGAAATCAA 387
122 oProThrPheGlyGlnGlyThrLysLeuGluIleLys 134
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seq\_name: /cgn2\_5/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-831-805A-10

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seq_documentation_block:
; Sequence 10, Application US/09831805A
; GENERAL INFORMATION:
; APPLICANT: INCYTE PHARMACEUTICALS, INC.
; APPLICANT: YUE, Henry
; APPLICANT: TANG, Y. Tom
; APPLICANT: CORLEY, Neil C.
; APPLICANT: GUEGLER, Karl J.
; APPLICANT: GORGONE, Gina A.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: LU, Dying Aina M.
; APPLICANT: LAL, Preeti
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: YANG, Junming
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0643 PCT
; CURRENT APPLICATION NUMBER: US/09/831,805A
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194
; PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PERL Program
; SEQ ID NO 10
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID NO: 3238787CD1
US-09-831-805A-10
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alignment\_scores:  
Quality: 594.50 Length: 130  
Ratio: 4.833 Gaps: 1  
Percent Similarity: 94.615 Percent Identity: 90.000

alignment\_block:

US-09-019-441-3 x US-09-831-805A-10

Align seg 1/1 to: US-09-831-805A-10 from: 1 to: 237

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1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17
51 CCAGAGTGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGCATCTGTAGGGACAGAGTCACCATCCTGAGCTCCTGGGGCTCCTCTGCTGGCT 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACCCAGGAAAGCTCTAA 200
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51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCTGATCTATGTTCATCCAGTTTCAAAGTGGGTCCCATCAAGGT 250
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67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTCGCACTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrThrPr 117
351 TCGG...ACGTTTCGCCCAAGGACCAAGTGGAAATCAA 387
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
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seq\_name: /cgn2\_5/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-107484

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seq_documentation_block:
; Sequence 107484, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Blonmix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107484
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-791-537-107484
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alignment\_scores:

Quality: 592.00 Length: 129  
Ratio: 4.933 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 89.922

alignment\_block:

US-09-019-441-3 x US-09-791-537-107484

Align seg 1/1 to: US-09-791-537-107484 from: 1 to: 135

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1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTCTGCTCTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17
51 CCAGAGTGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGCATCTGTAGGGACAGAGTCACCATCCTGAGCTCCTGGGGCTCCTCTGCTGGCT 150
|||||
34 erAlaSerValGlyAspArgValThrPheThrCysArgAlaSerGlnThr 50
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACCCAGGAAAGCTCTAA 200
|||||
51 IleAlaThrPheLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCTGATCTATGTTCATCCAGTTTCAAAGTGGGTCCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrGlyAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
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301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluAspPheAlaThrTyrCysGlnGlnSerTyrSerIlePr 117  
|  
351 TCGGACGTTCCGCCAAGGACCAAGGTGGAATCAAA 387  
|  
117 otrPrThrPheGlyGlnGlyThrLysValGluLeuLys 129

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-831-805A-1

seq\_documentation\_block:

; Sequence 1, Application US/09831805A  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE PHARMACEUTICALS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: TANG, Y. Tom  
; APPLICANT: CORLEY, Neil C.  
; APPLICANT: GUEGLER, Karl J.  
; APPLICANT: GORGONE, Gina A.  
; APPLICANT: BAUGHN, Mariah R.  
; APPLICANT: LU, Dyung Alina M.  
; APPLICANT: LAL, Preeti  
; APPLICANT: HILLMAN, Jennifer L.  
; APPLICANT: YANG, Junming  
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS  
; FILE REFERENCE: PF-0643 PCT  
; CURRENT APPLICATION NUMBER: US/09/831,805A  
; CURRENT FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 09/195,853; unassigned; 60/113,635; 60/128,194  
; PRIOR FILING DATE: 1998-11-19; 1998-11-19; 1998-12-22; 1999-04-07  
; NUMBER OF SEQ ID NOS: 38  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID NO: 079785CDI  
US-09-831-805A-1

alignment\_scores:  
Quality: 590.50 Length: 130  
Ratio: 4.801 Gaps: 1  
Percent Similarity: 94.615 Percent Identity: 89.231

alignment\_block:

US-09-019-441-3 x US-09-831-805A-1 ..

Align seg 1/1 to: US-09-831-805A-1 from: 1 to: 237

1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrrple 17  
51 CCCAGGTGCCAGATGTACATCCAGATGCCAGTCTCCATCTTCCCGT 100  
|  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34  
101 CTGCATCTGAGGGACAGTACCATCACTTCAGGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer 50  
151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCTCCTAA 200  
|  
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer 50  
151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCTCCTAA 200  
|  
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250  
|||||  
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84

251 TCAGCGCAGTGGATCTGGACACAGATTCACTCTCACCGTCAGCAGCGTG 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
|  
301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117  
|  
351 TCGG...ACGTTCGCCAAGGACCAAGGTGGAATCAAA 387  
|  
117 oProIleThrPheGlyGlnGlyThrArgLeuGluLeuLys 130

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-81820

seq\_documentation\_block:

; Sequence 81820, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 81820  
; LENGTH: 129  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-81820

alignment\_scores:  
Quality: 588.00 Length: 129  
Ratio: 4.820 Gaps: 0  
Percent Similarity: 94.574 Percent Identity: 88.372

alignment\_block:

US-09-019-441-3 x US-09-791-537-81820 ..

Align seg 1/1 to: US-09-791-537-81820 from: 1 to: 129

1 ATGGACATGAGGGTCCCGCTCAGCTCCTGGGGTCTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrrple 17  
51 CCCAGGTGCCAGATGTACATCCAGATGCCAGTCTCCATCTTCCCGT 100  
|  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34  
101 CTGCATCTGAGGGACAGTACCATCACTTCAGGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsn 50  
151 ATTAGGTATTATTTAAATTGGTATCAGCAGAAACCAGGAAAGCTCCTAA 200  
|  
51 IleIleSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGTCCCATCAAGGT 250  
|||||  
67 sLeuLeuMetTyrAlaAlaSerSerLeuGlnSerGlyValProAlaArgp 84  
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCGTG 300  
|  
84 heValGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnThrTyrSerAlaPr 117  
351 TCGGACGTTCCGCCAAGGACCAAGGTGGAATCAAA 387

[illegible]

; SEQ ID NO 65658  
; LENGTH: 131  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-791-537-65658

## alignment\_scores:

Quality: 581.00 Length: 131  
Ratio: 4.802 Gaps: 1  
Percent Similarity: 92.366 Percent Identity: 87.786

## alignment\_block:

US-09-019-441-3 x US-09-791-537-65658

Align seg 1/1 to: US-09-791-537-65658 from: 1 to: 131

1 ATGGACATGAGGTCCTCCGGCTCAGCTCTCTGGGGCTCTCTCTCTGGCT 50  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

1 MetAspThrArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriple 17

51 CCCAGGTGCCAGATGTCATCCAGATCCAGATCCAGATCCAGTCTCCCTGT 100  
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerLeus 34

101 CTGCATCTGTAGGGACAGAGTCACCATCTGTCAGGGCAAGTCAGGAC 150  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCAGGAAAGTCCTAA 200  
||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67

201 GCTCTGATCTATGTGTCATCCAGTTTCAAAGTGGGTCCCATCAAGGT 250  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

67 sleuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84

251 TCAGCGGAGTGATCTGGGACAGAGTTCTCTACCGTCAGCAGCGCTG 300  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCGTGAAGATTTTGGCACTTATTACTCTCTACAGTTTATAGTACCCC 350  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerProPr 117

351 T.....CGGACGTCGGCAAGGACCAAGTGGAATCAAA 387  
| ||||||| ||||||| ||||||| ||||||| ||||||| ||

117 oProValTyrThrPheGlyGlnGlyThrLysLeuGluIleLys 131

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-71040

## seq\_documentation\_block:

; Sequence 71040, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR

; FILE REFERENCE: 261/210

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 71040

; LENGTH: 210

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-791-537-71040

## alignment\_scores:

Quality: 578.50 Length: 130

Ratio: 4.781 Gaps: 1  
Percent Similarity: 93.077 Percent Identity: 89.231

## alignment\_block:

US-09-019-441-3 x US-09-791-537-71040

Align seg 1/1 to: US-09-791-537-71040 from: 1 to: 210

1 ATGGACATGAGGTCCTCCGGCTCAGCTCTCTGGGGCTCTCTCTCTGGCT 50  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuArgle 17

51 CCCAGGTGCCAGATGTCATCCAGATCCAGATCCAGTCTCCATCTTCCCTGT 100  
| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeus 34

101 CTGCATCTGTAGGGACAGATCCACCATCTGTCAGGGCAAGTCAGGAC 150  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50

151 ATTAGGTATTATTTAAATTTGGTATCAGCAGAAACCAGGAAAGTCCTAA 200  
||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67

201 GCTCTGATCTATGTGTCATCCAGTTTCAAAGTGGGTCCCATCAAGGT 250  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

67 sleuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84

251 TCAGCGGAGTGATCTGGGACAGAGTTCTCTACCGTCAGCAGCGCTG 300  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100

301 CAGCGTGAAGATTTTGGCACTTATTACTCTCTACAGTTTATAGTACCCC 350  
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||

101 GlnProGluAspPheAlaSerTyrTyrCysGlnGlnSerTyrArgThrPr 117

351 TCGG...ACGTTTCGGCAAGGACCAAGTGGAATCAAA 387  
| ||||||| ||||||| ||||||| ||||||| ||||||| ||

117 oAlaTrpThrPheGlyGlnGlyThrLysValGluIleLys 130

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-71830

## seq\_documentation\_block:

; Sequence 71830, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; FILE REFERENCE: 261/210

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 71830

; LENGTH: 127

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-791-537-71830

## alignment\_scores:

Quality: 578.00 Length: 124  
Ratio: 4.898 Gaps: 0  
Percent Similarity: 95.161 Percent Identity: 90.323

## alignment\_block:

US-09-019-441-3 x US-09-791-537-71830

Align seg 1/1 to: US-09-791-537-71830 from: 1 to: 127

16 CCCGCTCAGCTCCTGGGCTCTCTCTCTGGTCCCGAGGTGCCAGATG 65

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1  ProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuTrpLeuArgGlyAlaArgCy 17
66  TGACATCCAGATGACCCAGTCTCCATCTCCCTGCTCTGCATCTCTAGGGG 115
17  sAspIleGlnMetThrGlnSerProSerSerLeuSerAlaSerValGlyA 34
116 ACAGAGTCCACCATCAGTTCGAGGCAAGTCAGGACATTAGGTATTATTTA 165
34  sPArgValThrIleThrCysArgAlaSerGlnSerIleSerAsnTyrLeu 50
166 AATTGGTATCAGACAAACACGAGAAAGCTCTTAAGCTCCTGATCTATGT 215
51  AsnTrpTyrGlnArgLysProGlyLysAlaProLysLeuLeuIleTyrAl 67
216 TGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGTTTCAGCGGAGTGGAT 265
67  aAlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlyS 84
266 CTGGGACAGAGTTCACCTCTCACCTCAGCAGCTGCAGGCTGAAGATTTT 315
84  eRGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
316 GCGACTTATTACTCTCTACAGGTTTATGATACCCCTCGGACGTTTCGGCCA 365
101  AlathrTyTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyG 117
366 AGGGACCAAGGTGGAATCAAA 387
117  nGlyThrLysValGluIleLys 124

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB pep:US-09-791-537

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seq_documentation_block:
; Sequence 56448, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56448
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-56448

alignment_scores:
Quality: 578.00      Length: 124
Ratio: 4.898         Gaps: 0
Percent Similarity: 95.161      Percent Identity: 90.323

alignment_block:
US-09-019-441-3 x US-09-791-537-56448      ..

Align seg 1/1 to: US-09-791-537-56448 from: 1 to: 128

16  CCCGCTCAGCTCCCTGGGCTCCTTCTGCTGTGGCTCCAGTGCCAGATG 65
|||||
1  ProhlaGlnLeuLeuGlyLeuLeuLeuLeuLeuLeuArgGlyAlaArgCy 17

66  TGACATCCAGATGACCCAGTCTCCATCTTCCCTGCTGTCATCTGTAGGG 115
|||||
17  sAspIleGlnMethrGlnSerProSerSerLeuSerAlaSerValGlyA 34

116 ACAGAGTCACCATCATTGCGAGGCAAGTCAGGACATTAGGTATTATTA 165
|||||

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34  sPArgValThrIleThrCysArgAlaSerGlnSerAsnTyrLeu 50
166  AATTGGTATCAGCAGAAACAGGAAAGCTCTTAAGCTCCTGATCATGT 215
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
51  AsnTrpTyrGlnArgLysProGlyLysAlaProLysLeuIleTyrAl 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
216  TGCATCCAGTTTGCAAAAGTGGGTCCCATCAAGGTTTCAGCGCAGTGAT 265
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67  aAlaSerSerLeuGlnSerGlyValProSerArgPheSerGlySerGlyS 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
266  CTGGGACAGAGTTCACTCTCACGCTCAGCAGCTCGAGCCTGAAGATTTT 315
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84  erGlyThrAspPheThrLeuThrIleSerSerLeuGlnProGluAspPhe 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
316  GCGACTTATTACTCTCTACAGGTTTATAGTACCCCTCGAGCGTTCGGCCA 365
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101  AlaThrTyrTyrCysGlnGlnSerTyrAsnThrProTrpThrPheGlyGl 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
366  AGGGACCAAGGTGGAAATCAAA 387
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117  nGlyThrLysValGluIleLys 124
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep.US-09-791-537-107469

seq_documentation_block:
; Sequence 107469, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIE
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 107469
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-107469

alignment_scores:
Quality: 578.00 Length: 129
Ratio: 4.817 Gaps: 0
Percent Similarity: 93.023 Percent Identity: 88.372

alignment_block:
US-09-019-441-3 x US-09-791-537-107469 ..

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Align seg 1/1 to: US-09-791-537-107469 from: 1 to: 129

1 ATGGACATGAGGTCCTCCGCTCAGCTCTCTGGGGCTCTTCTGCTCTGGCT 50
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1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriPle 17
51 CCAGGTGCCAGATGTACATCCAGATGACCCAGCTCTCCATCTTCCCTGT 100
|||||
17 uArgGlyAlaArGcyAsPleGlnMetThrGlnSerProSerSerLeuS 34
101 CTGCATCTCTAGGGGACAGAGTCACCATCATCTTCGAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
|||||
151 ATTAGGTATTATTAAATTCGTATCAGCAGAAACCCAGGAAAGCTCTCAA 200
|||||
51 lleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67
201 GTCCTGTATCTATGTTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrAlaAlaSerLeuGlnSerGlyValThrSerArgp 84

```

251 TCACGGCAGTGGATCTGGACAGAGTTCACTCTACCGCTCAGCAGCGTG 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
|||||  
301 CAGCCTGAAGATTTTGGAGCTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluaspSerAlaThrTyrTyrCysGlnGlnSerTyrSerThrLe 117  
|||||  
351 TCGGACGTTTCGGCCAGGACCAAGGTGGAATCAAA 387  
|||||  
117 uileThrPheGlyGlnGlyThrArgLeuGluileLys 129

seq\_name: /cgn2\_5/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-74071

seq\_documentation\_block:  
; Sequence 74071, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 74071  
; LENGTH: 130  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-74071

alignment\_scores:  
Quality: 578.00 Length: 129  
Ratio: 4.817 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 88.372

alignment\_block:  
US-09-019-441-3 x US-09-791-537-74071 ..  
Align seg 1/1 to: US-09-791-537-74071 from: 1 to: 130

1 ATGACATGAGGTCCTCCGCTCAGCTCCTGGGCTCCTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17  
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGCTCCCATCTTCCCTGT 100  
1 |||||  
17 uArgGlyAlaArgCysaspIleGlnMetThrGlnSerProSerSerLeuS 34  
101 CTGCATCTGTAGGGACAGATGACCATCCATCTTCCAGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50  
151 ATTAGGTATTATTAAATGGTATATGATACAGAAACACAGAAAGCTCTAA 200  
|||||  
51 IleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GCTCTGATCTATGTTGCATCCAGTTTGCRAAGTGGGGTCCCATCAAGGT 250  
|||||  
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValThrSerArgp 84  
251 TCACGGCAGTGGATCTGGACAGAGTTCACTCTCACCGCTCAGCAGCGTG 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTTGGAGCTTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluaspSerAlaThrTyrTyrCysGlnGlnSerTyrSerThrLe 117

351 TCGGACGTTTCGGCCAGGACCAAGGTGGAATCAAA 387  
|||||  
117 uileThrPheGlyGlnGlyThrArgLeuGluileLys 129



Search time (sec): 70.150000

Sequence	Strd Orig	ZScore	EScore	Len
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/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-157-101A-2 +	551.00	1107.01	129 !
/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-470-139-26 +	534.00	1078.43	1,5e-54
/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-347-061-26 +	534.00	1078.43	1,5e-52
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-08-569-147-80 +	530.00	1070.29	3,1e-52
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-09-136-315-8 +	520.00	1050.01	4,2e-51
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-08-569-147-78 +	519.00	1047.90	5,4e-51
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-259-372A-14 +	518.00	1045.87	7,0e-51
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-468-671-14 +	518.00	1045.87	7,0e-51
/cgn2_6/ptodata/2/iaa/6A.COMB	pep:US-08-836-561-71 +	516.00	1041.87	1,2e-50
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-08-976-183A-46 +	511.00	1030.88	4,5e-50
/cgn2_6/ptodata/2/iaa/6A.COMB	pep:US-08-812-586-16 +	511.00	1025.64	5,1e-50
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-08-579-378A-18 +	508.00	1025.29	9,6e-50
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-461-284-2 +	506.00	1021.07	1,6e-49
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-462-939-2 +	506.00	1021.07	1,6e-49
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-253-877C-2 +	506.00	1021.07	1,6e-49
/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-452-164A-2 +	506.00	1021.07	1,6e-49
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/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-253-877C-28 +	505.50	1020.05	1,9e-49
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/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-379-057-29 +	496.00	1002.76	2,1e-48
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/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-378-939-24 +	493.00	996.66	4,6e-48
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-053-131-185 +	491.00	991.88	7,9e-48
/cgn2_6/ptodata/2/iaa/5B.COMB	pep:US-08-096-762-185 +	491.00	991.88	7,9e-48
/cgn2_6/ptodata/2/iaa/6A.COMB	pep:US-08-933-983-17 +	491.00	990.99	8,1e-48
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/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-09-025-769B-43 +	490.00	990.46	1,0e-47
/cgn2_6/ptodata/2/iaa/6A.COMB	pep:US-08-836-561-92 +	490.00	988.96	1,0e-47
/cgn2_6/ptodata/2/iaa/6B.COMB	pep:US-09-450-520A-6 +	490.00	988.88	1,0e-47
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/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-276-852-105 +	487.00	984.54	2,2e-47
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-899-575-105 +	487.00	984.54	2,2e-47
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-899-575-105 +	487.00	984.54	2,2e-47
/cgn2_6/ptodata/2/iaa/5A.COMB	pep:US-08-899-575-105 +	487.00	984.54	2,2e-47

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67 sleuMetIleTyrLysAlaSerIleLeuGluAsnGlyValProSerArgp 84  
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251 TCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300  
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84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerLeu 100  
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101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrLysSerTyrPr 117  
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351 TCGGAGCTTCGGCAAGGACCAAGGTGGAATCAAA 387  
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117 otrpThrPheGlyGlnGlyThrLysValGluIleLys 129  
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seq\_name: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:US-08-157-101A-5

seq\_documentation\_block:  
; Sequence 5, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
; TITLE OF INVENTION: PLASMIDS THEREFOR  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARLANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELE: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 236 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-157-101A-5

alignment\_scores:  
Quality: 551.00 Length: 129  
Ratio: 4.669 Gaps: 0  
Percent Similarity: 91.473 Percent Identity: 82.946  
alignment\_block:  
US-09-019-441-3 x US-08-157-101A-5 ..

Align seg 1/1 to: US-08-157-101A-5 from: 1 to: 236  
1 ATGACATGAGGTCCTCGGCTCAGCTCCTGGGGCTCTCTCTGCTGCT 50  
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1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17  
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51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100  
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17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerAlaMeta 34  
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101 CTGCATCTGTAGGACAGAGTCCACCATCACTTCAGCGGCAAGTCAGAC 150  
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34 IaAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50  
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151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACAGGAAAAGCTCTAA 200  
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51 IleGlyAsnTyrLeuValTrpPheGlnGlnLysProGlyLysValProLy 67  
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201 GCTCTGATCTATGTCATCCAGTTTGCAGAGTGGGTCCCATCAAGGT 250  
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67 sArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84  
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251 TCAGCGGAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300  
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84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerArgLeu 100  
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301 CAGCCTGAAGATTTGCGACTTATCTACTGCTACAGGTTTATAGTACCCC 350  
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101 GlnProGluAspPheAlaThrTyrTyrCysLeuHisAsnAsnTyrPr 117  
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351 TCGGAGCTTCGGCAAGGACCAAGGTGGAATCAAA 387  
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seq\_name: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:US-08-470-139-26

seq\_documentation\_block:  
; Sequence 26, Application US/08470139  
; Patent No. 5998586  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Interleukin-5 specific recombinant antibodies  
; NUMBER OF SEQUENCES: 28  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/470,139  
; FILING DATE: 06 JUNE-1995  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TRUJILLO, DOREEN YATKO  
; REGISTRATION NUMBER: 35,719  
; REFERENCE/DOCKET NUMBER: CARP-0044  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-470-139-26

alignment\_scores:  
Quality: 534.00 Length: 127  
Ratio: 4.643 Gaps: 0  
Percent Similarity: 90.551 Percent Identity: 81.102  
alignment\_block:  
US-09-019-441-3 x US-08-470-139-26 ..



Align seg 1/1 to: US-08-470-139-26 from: 1 to: 128

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seq\_name: /cqn2\_6/ptodata/2/iaa/6B\_COMB.pep:US-09-347-061-26

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seq_documentation_block:
; Sequence 26, Application US/09347061
; Patent No. 6316227
; GENERAL INFORMATION:
; APPLICANT: Bodmer, Mark
; APPLICANT: Athwal, Diljeet Singh
; APPLICANT: Emtage, John Spencer
; TITLE OF INVENTION: Interleukin-5 Specific Recombinant Antibodies
; FILE REFERENCE: CARP-0071
; CURRENT APPLICATION NUMBER: US/09/347,061
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: No. 6316227el Sequence
US-09-347-061-26

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alignment_scores:			
Quality:	534.00	Length:	127
Ratio:	4.643	Gaps:	0
Percent Similarity:	90.551	Percent Identity:	81.102

alignment\_block:

US-09-019-441-3 x US-09-347-061-26

Align seq 1/1 to: US-09-347-061-26 from: 1 to: 128

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34  erValGlyAspArgValThrIleThrCysLeuAlaSerGluGlyIleSer 50
    |||||
157 TATTATTAAATTGGTATCAGCAGAAACCCAGGAAAAGCTTCCTAAGCTCCT 206
    |||||
51  SerTyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLe 67
    |||||
207 GATCTATGTTGCATCCAGTTTGCANAAGTGGGGTCCCATCAGGTTTCAGG 256
    |||||
67  uIleTyrGlyAlaAsnSerLeuGlnThrThyValProSerArgPheSerG 84
    |||||
257 GCAGTCGATCTGGACAGAGTTCACTCTCACCGTCAGCAGGCTGCAGCCT 306
    |||||
84  lYserGlySerAlaThrAspIrrThrLeuThrIleSerSerLeuGlnPro 100
    |||||
307 GAAGATTTTCGCGATTATTACTGTCTACAGGTTTATAGTACCCCTCGGAC 356
    |||||
101 GluAspPheAlaThrTyrTyrCysGlnGlnSerTyrLysPheProAsnTh 117
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357 GTTCGCCCAAGGACCAAGGTGGAAATCAA 387
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117 rPheGlyGlnGlyThrLysValGluValLys 127

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seq\_name: /cqn2\_6/ptodata/2/iaa/6B\_COMB.pep:US-08-569-147-80

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seq_documentation_block:
: Sequence 80, Application US/08569147
: Patent No. 6180377
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: HUMANISED ANTIBODIES
: NUMBER OF SEQUENCES: 95
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: ADDRESSEE: No. 6180377ris, LLP
: STREET: One Liberty Place - 46th Floor
: CITY: Philadelphia
: STATE: PA
: COUNTRY: U.S.A.
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/569,147
: FILING DATE: 25-March-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Trujillo, Doreen Yatko
: REGISTRATION NUMBER: 35,719
: REFERENCE/DOCKET NUMBER: CARP-0047
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (215) 568-3100
: TELEFAX: (215) 568-3439
: INFORMATION FOR SEQ ID NO: 80:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 128 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-569-147-80

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alignment_scores:
  Quality: 530.00
  Length: 127
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Ratio: 4.569 Gaps: 0  
Percent Similarity: 91.339 Percent Identity: 81.102

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57 TGCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCAT 106
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17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAla 34

107 CTGTAGGGGACAGATCACCATCTTCAGGCAAGTCAGGACATTAGG 156
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34 erValGlyAspArgValThrIleThrCysArgAlaSerGluAsnIleTyr 50

157 TATTATTAAATTTGGTATCAGCAGAAACCCAGGAAAGCTCTAAGCTCCT 206
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51 AsnAsnLeuAlaTrpTyrGlnLysProGlyLysAlaProLysLeuLe 67

207 GATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCACGG 256
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67 uIleTyrAlaAlaThrAsnLeuAlaAspGlyValProSerArgPheSerG 84

257 GCACTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTGCAGCCT 306
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 LySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGlnPro 100

307 GAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAC 356
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GluAspPheAlaThrTyrTyrCysGlnHisPheTrpThrProTyrPal 117

357 GTTCGGCAAGGGACCAAGTGGAAATCAAA 387
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117 pHeGlyGlnGlyThrLysValGluIleLys 127
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seq\_name: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:US-09-136-315-8

## seq\_documentation\_block:

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; Sequence 8, Application US/09136315B
; Patent No. 6228360
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; TITLE OF INVENTION: ANTITHROMBOTIC AGENT AND HUMANIZED ANTI-VON WILLEBRAND
; FILE REFERENCE: 0010-0933-0
; CURRENT APPLICATION NUMBER: US/09/136,315B
; CURRENT FILING DATE: 1998-08-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:SYNTHETIC DNA
US-09-136-315-8
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## alignment\_scores:

Quality: 520.00 Length: 127  
Ratio: 4.483 Gaps: 0  
Percent Similarity: 91.339 Percent Identity: 77.953

## alignment\_block:

US-09-019-441-3 x US-09-136-315-8 ..

Align seg 1/1 to: US-09-136-315-8 from: 1 to: 127

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1 MetSerValProThrGlnValLeuGlyLeuLeuLeuTrpLeuThrAs 17

57 TGCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCAT 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAla 34

107 CTGTAGGGGACAGATCACCATCTTCAGGCAAGTCAGGACATTAGG 156
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34 erValGlyAspArgValThrIleThrCysArgAlaSerGluAsnIleTyr 50

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207 GATCTATGTTGCATCCAGTTTGCAAGTGGGGTCCCATCAAGTTCACGG 256
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67 uIleTyrAlaAlaThrAsnLeuAlaAspGlyValProSerArgPheSerG 84

257 GCACTGGATCTGGGACAGAGTTTCACTCTCACCGTCAGCAGCTGCAGCCT 306
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84 LySerGlySerGlyThrGlnTyrThrLeuThrIleSerSerLeuGlnPro 100

307 GAAGATTTTGGGACTTATTACTGTCTACAGTTTATAGTACCCCTCGGAC 356
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GluAspPheAlaThrTyrTyrCysGlnHisLeuTrpThrSerProTyrTh 117

357 GTTCGGCAAGGGACCAAGTGGAAATCAAA 387
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117 rPheGlyGlyThrLysValGluIleLys 127
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seq\_name: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:US-08-569-147-78

## seq\_documentation\_block:

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; Sequence 78, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Irujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 78:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-78
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Quality: 519.00 Length: 127  
Ratio: 4.474 Gaps: 0  
Percent Similarity: 91.339 Percent Identity: 78.740

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US-09-019-441-3 x US-08-569-147-78 ..

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1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrAs 17

57 TGCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGTCTGCAT 106  
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17 pAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuSerAlas 34

107 CTGTAGGGGACAGAGTACCATCACTTGCAGGGCAAGTCAGGACATTAGG 156  
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34 erValGlyAspArgValThrIleThrCysArgAlaSerGluAsnIleTyr 50

157 TATTATTTAAATGGTATCATCACGAACACAGAAAAGTCTTAAGCTCCT 206  
|||||.....  
51 SerAsnLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProGlnLeuLe 67

207 GATCTATGTTGCATCCAGTTGCCAAGTGGGGTCCCATCAAGTTCAGCG 256  
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67 uilePheAlaAlaSerAsnLeuAlaAspGlyValProSerArgPheSerG 84

257 GCAGTGGATCTGGACAGAGTTCACTCTCACCGTCAGCAGCTCGAGCCT 306  
|||||.....  
84 lySerGlySerGlyThrAspPheThrLeuThrIleThrSerLeuGlnAla 100

307 GAAGATTTTTGCGACTTATTACTGTCTACAGGTTTTATAGTACCCCTCGGAC 356  
|||||.....  
101 GluAspPheAlaThrTyrTyrCysGlnGlnAlaAspSerLeuProPheTh 117

357 GTTCGGCCAAGGACCAAGGTGGAAATCAA 387  
|||||.....  
117 apHeGlyGlnGlyThrLysValGluIleLys 127

seq\_name: /cgn2\_5/ptodata/2/iaa/5A\_COMB pep:US-08-259-372A-14

seq\_documentation\_block:  
Sequence 14, Application US/08259372A  
Patent No. 5565354  
GENERAL INFORMATION:  
APPLICANT: Ostberg, Lars G.  
TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/259,372A  
FILING DATE: 14-JUN-1994  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/871,426  
FILING DATE: 21-APR-1992





357 GTTCGCCAAGGACCAAGCTGGAATCAAA 387  
|||||  
124 rPheGlyGlnGlyThrLysValGluValLys 134

seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-812-586-16

seq\_documentation\_block:

; Sequence 16, Application US/08812586

; Patent No. 6048704

; GENERAL INFORMATION:

; APPLICANT: Martin David Tilson

; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC

; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURISM (AAA)

; TITLE OF INVENTION: DISSEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham LLP

; STREET: 1185 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/812,586

; FILING DATE: 07-MAR-1997

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 0575/53862-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 278-0400

; TELEFAX: (212) 391-0525

; INFORMATION FOR SEQ ID NO: 16:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-812-586-16

alignment\_scores:

Quality: 511.00 Length: 129

Ratio: 4.482 Gaps: 0

Percent Similarity: 88.372 Percent Identity: 77.519

alignment\_block:

US-09-019-441-3 x US-08-812-586-16

Align seg 1/1 to: US-08-812-586-16 from: 1 to: 235

1 ATGCACATGAGGTCGCCGCTCAGCTCCTGGGGCTCCTCTGCTGGCT 50

1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

51 CCCAGGTGCCAGATGTGCATCCAGATGACCCAGTCTCCATCTCCCTGT 100

17 uProGlyAlaArgCysAlaIleargIleAlaGlnSerProSerSerLeu 34

101 CTGCATCTGTAGGGACAGAGTCCACCATCTGTCAGGGCAAGTCAGGAC 150

34 erAlaSerThrGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50

151 ATTAGGTATTATTATTGGTATCAGCAGAAACACGAGAAAGCTCTAA 200

51 IleSerAsnTyrLeuAlaTrpTyrGlnGlnLysProGlyGlnAlaProAr 67

201 GCTCCTGATCTATGTCATCCAGTTCGAAAGTGGGTCCCATCAAGGT 250  
:|||||  
67 gLeuLeuIleTyrAspAlaSerSerArgAlaThrGlyIleProAspArgP 84

251 TCAGGGCAGTGGATCTGGGACAGAGTTCACCTCAGCGTCAGCAGCCTG 300

84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerArgLeu 100

301 CAGCCTGAAGATTTGGCAGCTTATCTACTGTCTACAGGTTTATAGTACCC 350

101 GluProGluAspPheAlaValTyrTyrGlyGlnGlnTyrGlySerSerP 117

351 TCGGACGTTTCGCGCAAGGACCAAGTGGGAATCAAA 387

117 oLeuThrPheGlyGlyThrLysValGluIleLys 129

seq\_name: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:US-08-579-378A-18

seq\_documentation\_block:

; Sequence 18, Application US/08579378A

; Patent No. 6210671

; GENERAL INFORMATION:

; APPLICANT: Co. Man Sung

; TITLE OF INVENTION: Humanized Antibodies Reactive with

; TITLE OF INVENTION: L-Selectin

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew

; STREET: One Market Plaza, Steuart Tower, Suite 2000

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94105

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/579,378A

; FILING DATE: 27-DEC-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/160,074

; FILING DATE: 30-NOV-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/983,946

; FILING DATE: 01-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95112895.8

; FILING DATE: 17-AUG-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: EP 95114696.8

; FILING DATE: 19-SEP-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Liebeschütz, Joe O.

; REGISTRATION NUMBER: 37,505

; REFERENCE/DOCKET NUMBER: 11823-002220

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 18:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 131 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-579-378A-18

alignment\_scores:

Quality: 508.00

Length: 131

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Ratio: 4.379 Gaps: 1
Percent Similarity: 88.550 Percent Identity: 75.573

alignment_block:
US-09-019-441-3 x US-08-579-378A-18 ..
Align seg 1/1 to: US-08-579-378A-18 from: 1 to: 131

7 ATGAGGTCCTCCGCTAGCTCTGGGCTCCTTCTGCTGTGGTCCAGG 56
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MetGluThrAspThrIleLeuLeuTrpValLeuLeuLeuTrpValProG1 17
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
57 TGCAGATGTGACATCAGATGACCCAGTCCATCTCCATCTTCCCTGCTGCAT 106
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
17 ySerThrGlyAspIleGlnMetThrGlnSerProSerSerLeuSerAlas 34
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
107 CTGTAGGGGACAGATCACCATCCTTGCAGGCAAGTCAGGACATTAGG 156
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
34 erValGlyAspArgValThrIleThrCysLysAlaSerGlnSerValAsp 50
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
157 TAT.....TATTAAATTGGTATCAGACAGATTCAGGAAAGC 194
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
51 TyrAspGlyAspSerTyrMetAsnTrpTyrGlnGlnLysProGlyLysAl 67
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
195 TCCTAAGCTCCTGATCTATCTGTCATCCACTTGCAGGCAAGTGGGTCCAT 244
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
67 aProLysLeuLeuIleThrIleThrAlaAlaSerAsnLeuGluSerGlyIleProS 84
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
245 CAAGGTTACAGCGCAGTGGATCTGGGACAGATTCACCTCAGCGTCAGC 294
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
84 erArgPheSerGlySerGlySerGlyThrAspPheThrLeuThrIleSer 100
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
295 AGCTTCAGCGCTGAAGATTTTGGCATTATTACTGTCTACAGGTTTATAG 344
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
101 SerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerAsnG1 117
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
345 TACCCCTCGCAGCTCGGCCAAGGCAAGTGGGAATCAAA 387
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
117 uAspProTrpThrPheGlyGlnGlyThrLysValGluLeuLys 131
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-461-284-2

seq_documentation_block:
; Sequence 2, Application US/08461284
; Patent No. 5739116
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
; TITLE OF INVENTION: Conjugates of Methyltrithio Antitumor
; AGENTS AND INTERMEDIATES FOR THEIR SYNTHESIS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,284
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
```

```
APPLICATION NUMBER: US 08/253,877
FILING DATE: 03-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jackson, Herbert G.
REGISTRATION NUMBER: 24,476
REFERENCE/DOCKET NUMBER: 32,368
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3142
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-461-284-2

alignment_scores:
Quality: 506.00 Length: 131
Ratio: 4.325 Gaps: 1
Percent Similarity: 89.313 Percent Identity: 74.809

alignment_block:
US-09-019-441-3 x US-08-461-284-2 ..
Align seg 1/1 to: US-08-461-284-2 from: 1 to: 133

7 ATGAGGTCCTCCGCTAGCTCTGGGCTCCTTCTGCTGTGGTCCAGG 56
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
1 MetSerValProThrGlnValLeuGlyLeuLeuLeuLeuTrpLeuThrAs 17
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
57 TGCAGATGTGACATCAGATGACCCAGTCTCCATCTTCCCTGCTGCAT 106
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
17 pAlaArgCysAspIleGlnLeuThrGlnSerProSerThrLeuSerAlas 34
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
107 CTGTAGGGGACAGATCACCATCCTTGCAGGCAAGTCAGGACATTAGG 156
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
34 erValGlyAspArgValThrIleThrCysArgAlaSerGlnSerLeuAsp 50
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
157 TATTAT.....TTAAATTGGTATCAGCAGAAACAGGAAAGC 194
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
51 AsnTyrGlyIleArgPheLeuThrTrpPheGlnGlnLysProGlyLysAl 67
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
195 TCCTAAGCTCCTGATCTATCTGTCATCCAGTTCGAAAGTGGGTCCAT 244
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
67 aProLysLeuLeuMetTyrAlaAlaSerAsnGlnGlySerGlyValProS 84
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
245 CAAGGTTACAGCGCAGTGGATCTGGGACAGATTCACCTCAGCGTCAGC 294
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
84 erArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSer 100
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
295 AGCTTCAGCGCTGAAGATTTTGGCATTATTACTGTCTACAGGTTTATAG 344
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
101 SerLeuGlnProAspPheAlaThrTyrTyrCysGlnGlnThrLysG1 117
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
345 TACCCCTCGCAGCTTCGCCAAGGCAAGTGGGAATCAAA 387
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :
117 uValProTrpSerPheGlyGlnGlyThrLysValGluValLys 131
|||||: : : : : : : : : : : : : : : : : : : : : : : : : : :

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-462-939-2

seq_documentation_block:
; Sequence 2, Application US/08462939
; Patent No. 5767285
; GENERAL INFORMATION:
; APPLICANT: Hamann, Philip R.
; APPLICANT: Hinman, Lois
; APPLICANT: Hollander, Irwin
; APPLICANT: Holcomb, Ryan
; APPLICANT: Hallett, William
; APPLICANT: Tsou, Hwei-Ru
; APPLICANT: Weiss, Martin J.
```

; TITLE OF INVENTION: Conjugates of Methylthio Antitumor
; TITLE OF INVENTION: Agents and Intermediates for Their Synthesis
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: American Cyanamid Company
; STREET: One Cyanamid Plaza
; CITY: Wayne
; STATE: New Jersey
; COUNTRY: United States
; ZIP: 07470-8426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/462,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/253,877
; FILING DATE: 03-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson, Herbert G.
; REGISTRATION NUMBER: 24,476
; REFERENCE/DOCKET NUMBER: 32,368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-831-3142
; TELEFAX: 201-831-3305
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-462-939-2

alignment\_scores:
Quality: 506.00 Length: 131
Ratio: 4.325 Gaps: 1
Percent Similarity: 89.313 Percent Identity: 74.809

alignment\_block:
US-09-019-441-3 x US-08-462-939-2 ..

Align seg 1/1 to: US-08-462-939-2 from: 1 to: 133

7 ATGAGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTGCTGCCAGG 56
||| |||||:|||||:|||||:|||||:|||||:|||||:
1 MetSerValProThrGlnValLeuGlyLeuLeuLeuTrpLeuThrAs 17

57 TGCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGTCTGCAT 106
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 pAlaArgCysAspIleGlnLeuThrGlnSerProSerThrLeuSerAlas 34

107 CTGTAGGGGACAGTCACCATCCTTGCAGGCAAGTCAGGACATTAGG 156
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
34 erValGlyAspArgValThrIleThrCysArgAlaSerGluSerLeuAsp 50

157 TATTAT.....TTAAATTGGTATCAGAGAAACAGGAAAGC 194
||| |||||:|||||:|||||:|||||:|||||:
51 AsnTyrGlyIleArgPheLeuThrTrpPheGlnGlnLysProGlyLysAl 67

195 TCCTAAGCTCCTGATCTATGTCATCCAGTTTGCAAAGTGGGGTCCCAT 244
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
67 apProLysLeuLeuMetTyrAlaAlaSerAsnGlnGlySerGlyValPro 84

245 CAAGTTTCAGCGGCTGATCTGGGACAGAGTTTCACTCTCACCCTCAGC 294
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 erArgPheSerGlySerGlySerGlyThrGluPheThrLeuThrIleSer 100

295 AGCCTGCAGCCTGAAGATTTTGGCGACTTATTACTGTCTACAGGTTTATAG 344

|||||:|||||:|||||:|||||:|||||:|||||:|||||:
101 SerLeuGlnProAspAspPheAlaThrTyrTyrCysGlnGlnThrLysG1 117

345 TACCCTCGGACGTTTCGGCCAAAGGACCAAGGTGGAATCAA 387
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
117 uValProTrpSerPheGlyGlnGlyThrLysValGluValLys 131



F;34-TT//DonaII: IIIIIIIOGTOBUTIII IOIIOIOIOY <ITM>

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seq\_name: pir2:S05271

seq\_documentation\_block:  
Ig heavy chain precursor - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 16-Aug-1996  
C:Accession: S05271; S04602  
R:Kishimoto, T.  
submitted to the EMBL Data Library, March 1989

A:Reference number: S05270

A:Accession: S05271

A:Molecule type: mRNA

A:Residues: 1-160 <KIS1>

A:Cross-references: EMBL:X14584

R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of

A:Reference number: S04601; MUID:89296497

A:Accession: S04602

A:Molecule type: mRNA

A:Residues: 1-144 <KIS2>

A:Cross-references: EMBL:X14584

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:

Quality: 538.50 Length: 146

Ratio: 4.308 Gaps: 2

Percent Similarity: 85.616 Percent Identity: 72.603

alignment\_block:

US-09-019-441-4 x S05271 ..

Align seg 1/1 to: S05271 from: 1 to: 160

1 ATGGAGTTTGGCTGAGCTGGTGGTTTCCTCTCTCTTTTGAAGGTGT 50  
|||||

1 MetGluPheGlyLeuSerTrpPheLeuValAlaIleLeuLysGlyVa 17  
|||||

51 CCAGTGTGAGTGGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTG 100  
|||||

17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34  
|||||

101 GGGGGTCCCTGAGACTCTGGTGGCGAGCTCCGGGTTCCAGGTTCCACCTTC 150  
|||||

34 lYgYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
|||||

151 AATAACTACTACATGAGCTGGTGGTCCGACGCTCCAGGGCGAGGCTGGA 200  
|||||

49 SerThrTyraMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65  
|||||

201 GTGGGCTCAGCTATTAGTAGTGTGATCCACATGTTACGACGACT 250  
|||||

65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrrAlaAsps 82  
|||||

251 CCGTAGAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300  
|||||

82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
|||||

301 TTTCTTCAATGAACACCTGAGAGCTGAGACACGCTGTCTATTACTG 350  
|||||

99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrrCy 115  
|||||

351 TGGCAGCTTGACTACA.....GGGTCGTG 373  
|||||

115 sAlaLysAlaValArgGlyValIleSerTyrrTyrrTyrrGlyMeta 132  
|||||

374 ACTCCTGGGCGAGGAGTCTGGTACCGCTCTCCTCA 411  
|| |||||

seq\_documentation\_block:  
Ig heavy chain V region - human (fragment)

132 spValTrpGlyGlnGlyThrThrValThrValSerSer 144

seq\_name: pir2:S31686

seq\_documentation\_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31686

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

A:Reference number: S31585

A:Accession: S31686

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

A:Cross-references: EMBL:Z14205; NID:930969; PIDN:CAA78574.1; PID:930970

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:

Quality: 529.50 Length: 142

Ratio: 4.202 Gaps: 3

Percent Similarity: 88.732 Percent Identity: 74.648

alignment\_block:

US-09-019-441-4 x S31686 ..

Align seg 1/1 to: S31686 from: 1 to: 140

1 ATGGAGTTTGGCTGAGCTGGTGGTTTCCTCTCTCTTTTGAAGGTGT 50  
|||||

1 MetGluPheGlyLeuSerTrpPheLeuValAlaIleLeuLysGlyVa 17  
|||||

51 CCAGTGTGAGTGGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTG 100  
|||||

17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34  
|||||

101 GGGGGTCCCTGAGACTCTGGTGGCGAGCTCCGGGTTCCAGGTTCCACCTTC 150  
|||||

34 lYgYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
|||||

151 AATAACTACTACATGAGCTGGTGGTCCGACGCTCCAGGGCGAGGCTGGA 200  
|||||

49 SerThrTyraMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65  
|||||

201 GTGGGCTCAGCTATTAGTAGTGTGATCCACATGTTACGACGACT 250  
|||||

65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrrTyrrSerAsps 82  
|||||

251 CCGTAGAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300  
|||||

82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
|||||

301 TTTCTTCAATGAACACCTGAGAGCTGAGACACGCTGTCTATTACTG 350  
|||||

99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrrCy 115  
|||||

351 TGGCAGC.....TTGACTACAGGCTCT.....GACTCTGGGGGCC 385  
|||||

115 sAlaLysCysProPheAlaGlyGlySerProSerPheAspTyrrTrpGlyG 132  
|||||

386 AGGAGTCTCTGGTCCCGTCTCCTCA 411  
|||||

132 lnglyThrLeuValThrValSerSer 140  
|||||

seq\_name: pir2:S31588

seq\_documentation\_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31588  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31588  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140 <CUI>  
A:Cross-references: EMBL:214200; NID:g30957; PIDN:CAA78569.1; PID:g30958  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 528.50 Length: 142  
Ratio: 4.262 Gaps: 2  
Percent Similarity: 87.324 Percent Identity: 73.944

alignment\_block:

US-09-019-441-4 x S31588 ..

Align seg 1/1 to: S31588 from: 1 to: 140

```
1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuArgGlyVa 17
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCTG 100
|||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCCTCCTGAGACTCTGGTGGCGCAGCTCCGGGTTTCAGGTTTCCACCTTC 150
|||||
34 lYGLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGTGGTGGTCCGCGAGGCTCCAGGGCAGGGCTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
201 GTGGGTCCTCAGTATTAGTAGTCTGATCCACATGTTGATCCAGCT 250
|||||
65 utrPValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsp 82
251 CCGTGAAGGGCAGATTCCACATCTCCAGAGAGAACGCCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAspSerLysAsnThrLeu 98
301 TTTCTTCAAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGGCAGCTTGACTACAGGCTCT.....GACTCTGGGGCC 385
|||||
115 sAlaArg...TrpArgAspLeuAspTyrIleTyrPheAspTyrTrpGlyG 132
386 AGGAGTCTGGTCCAGCTCTCCCTCA 411
|||||
132 lNGlyThrLeuValThrValSerSer 140
```

seq\_name: pir2:S31588

seq\_documentation\_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31588

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from the

A:Reference number: S31585  
A:Accession: S31699  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-134 <CUI>  
A:Cross-references: EMBL:214201; NID:g30961; PIDN:CAA78570.1; PID:g30962  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:

Quality: 526.50 Length: 137  
Ratio: 4.351 Gaps: 2  
Percent Similarity: 88.321 Percent Identity: 75.912

alignment\_block:

US-09-019-441-4 x S31699 ..

Align seg 1/1 to: S31699 from: 1 to: 134

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1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCTG 100
|||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValHisProG 34
101 GGGGTCCTCCTGAGACTCTGGTGGCGCAGCTCCGGGTTTCAGGTTTCCACCTTC 150
|||||
34 lYGLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGTGGTGGTCCGCGAGGCTCCAGGGCAGGGCTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
201 GTGGGTCCTCAGTATTAGTAGTCTGATCCACATGTTGATCCAGCT 250
|||||
65 utrPValSerAlaIleSerGlySerGlyGlySerThrTyrTyrSerAsp 82
251 CCGTGAAGGGCAGATTCCACATCTCCAGAGAGAACGCCCAACACACTG 300
|||||
82 erValLysGlyArgLeuThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGGCAGCTTGACTACAGGCTCTGACTCTGGGGCGGAGGAGCTCTGTGTC 400
|||||
115 sAlaArg...TrpArgAspLeuAspTyrTrpGlyGlnGlyThrLeuValT 131
401 CCGTCTCTCTCA 411
|||||
131 hrValSerSer 134
```

seq\_name: pir2:S70442

seq\_documentation\_block:

Ig heavy chain precursor V region (mu) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 24-Jul-1998 #sequence\_revision 24-Jul-1998 #text\_change 21-Jan-2000

C:Accession: S70442

R:Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelles, C.

Mol. Immunol. 29, 1363-1373, 1992

A:Title: Igm kappa/Lambda EBV human B cell clone: an early step of differentiation of

A:Reference number: S70442; MUID:93024508

A:Accession: S70442

A:Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-140 <CUI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 518.00 Length: 141  
Ratio: 4.281 Gaps: 2  
Percent Similarity: 85.816 Percent Identity: 73.759

alignment\_block:  
US-09-019-441-4 x S70442 ..

Align seg 1/1 to: S70442 from: 1 to: 140

1 ATGGAGTTGGCTGAGCTGGGTTTCCTTCTCTCTTTCAAGGCTG 50  
|||||  
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17  
51 CCAAGTGTGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100  
|||||  
17 LgInCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34  
101 GGGGTCTCCTGAGACTCTGGTGGCGAGCTCGGGTTTCAGGTTCACCTTC 150  
|||||  
34 LgGlySerLeuArgLeuSerCysAlaLaSerGly.....PheThrPhe 48  
151 AATACTACTACATGACTGGTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200  
|||||  
49 SerAsnTyrGlyMeHisTrpValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGTCTCAGCTATTACTAGTGTGATCCACATGGTACGCGAGCT 250  
|||||  
65 uTrpValAlaPheIleAlaGlyTyrAspGlySerAsnLysTyrTyrAlaAspS 82  
251 CCGTCAAGGGCAGATTACCATCTCCAGAGAGAGAGAGAGAGAGAGAGAG 300  
|||||  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTTCTTCAATGACAGCTGAGAGCTGAGAGCTGAGAGAGAGAGAGAGAGAG 350  
|||||  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115  
351 TCGAGC.....TTGACTACAGGCTGACTCTCTCTCTCTCTCTCTCTCA 411  
|||||  
115 sAlaArgAspHisIleValGlyAlaThrTyrPheAspTyrTrpGlyGlnG 132  
389 GAGTCTCTGGTCCAGCTCTCTCTCA 411  
|||||  
132 LyrThrLeuValThrValSerSer 139

seq\_name: pir2:S31587

seq\_documentation\_block:  
Ig heavy chain V region - human  
C:Species: Homo sapiens (man)  
C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S31587  
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelles, C.  
submitted to the EMBL Data Library, June 1992  
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the  
A:Reference number: S31585  
A:Accession: S31587  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-136 <CU>  
A:Cross-references: EMBL:Z14189; NID:g31005; PIDN:CAA78558.1; PID:g31006  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-114/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 517.00 Length: 138  
Ratio: 4.169 Gaps: 2

Percent Similarity: 89.855 Percent Identity: 72.464

alignment\_block:  
US-09-019-441-4 x S31587 ..

Align seg 1/1 to: S31587 from: 1 to: 136

10 GGGCTGAGCTGGTTCCTTCTCTCTTTTAAAGGTGTCCAGTGTGA 59  
|||||  
1 GlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyValGlnCysG 17  
60 GGTGACGCTGGAGTCTGGGGGGGCTTGGCAAAGCCTGGGGGTGCC 109  
|||||  
17 uValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySerL 34  
110 TCAGACTCTGGTGGCGAGCTCCGGTTCAGGTTCACCTTCAATAACTAC 159  
|||||  
34 euArgLeuSerCysAlaLaSerGly.....PheThrPheSerTyr 48  
160 TACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTCTC 209  
|||||  
49 TrpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValAl 65  
210 ACGTATTAGTACTAGTGTGATCCACATGGTACGACACTCCGTGAAG 259  
|||||  
65 asnIleLysGlnAspGlySerGluLysTyrTyrValAspSerValLysG 82  
260 GCAGATTCCATCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 309  
|||||  
82 LyrArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuGln 98  
310 ATGAACACCTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 359  
|||||  
99 MetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArgG 115  
360 GACTACAGGGTCT.....GACTCTCTGGGGCCAGGAGTCTCTGG 397  
|||||  
115 yLeuThrGlyAlaThrAspAlaPheAspIleTrpGlyGlnGlyThrMetV 132  
398 TCACCGTCTCTCTCA 411  
|||||  
132 alThrValSerSer 136

seq\_name: pir2:A60943

seq\_documentation\_block:  
Ig heavy chain precursor V region (clone HN.14) - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 17-Mar-1999  
C:Accession: A60943; A48165  
R:Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.  
J. Neuroimmunol. 30, 245, 1990  
A:Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) regio  
A:Reference number: A60943; MUID:91036050  
A:Accession: A60943  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-151 <DE>  
R:Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.; Alt, F.W.; Kabat, E.A.  
J. Neuroimmunol. 26, 35-41, 1990  
A:Title: Molecular cloning of a human immunoglobulin heavy chain variable (V-H) regio  
A:Reference number: A48165; MUID:90094677  
A:Accession: A48165  
A:Molecule type: mRNA  
A:Residues: 1-136, 'M', 38-62, 'AR', 67-151 <DE>  
A:Note: this sequence has been corrected in reference A60943  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

alignment\_scores:  
Quality: 517.00 Length: 145



```
|||||
19 ncysGluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyG 36
|||||
104 GTCCCTGAGACTCTGGTGGCGAGCCTCCGGGTTCAGGTTACACCTCAAT 153
|||||
36 lySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPheSer 50
154 RACTACTACATGAGCTGGTCCGCCAGCTCCAGGCGAGGGCTGGAGTG 203
|||||
51 SerTyrTrpMetSerTrpValArgGlnLeuProGlyLysGlyLeuGluTr 67
204 GGTCTCAGCTATTAGTACTAGTGGTGATCCACATGGTACGAGACTCCG 253
|||||
67 pValAlaAsnIleLysGlnAspGlySerGluLysTyrTrpValAspSerV 84
254 TGAAGGCGAGATTACCATCTCCAGAGAGAAGCCAAACACACACTGTT 303
|||||
84 aLLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTr 100
304 CTTCAAATGAACAGCTGAGAGCTGAGACAGCGCTGTCTATTACTGTGC 353
|||||
101 LeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAl 117
354 GAGCTTGACTACAGGCTCT.....GACTCTCGGGGCCAGGAGTCC 394
|||||
117 aArgLysArgAlaGlyLysAlaAlaPheAsnIleTrpGlyGlnGlyThrm 134
395 TGGTCACCGTCTCCTCA 411
|||||
134 etValThrValSerSer 139
```

seq\_name: pir2:S22657

seq\_documentation\_block:

Ig heavy chain precursor V region (0-81VH) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 06-Feb-1998

C:Accession: S22657

R:Hirabayashi, Y.; Munakata, Y.; Sasaki, T.; Sano, H.

Nucleic Acids Res. 20, 2601, 1992

A:Title: Variable regions of a human anti-DNA antibody O-81 possessing lupus nephritis-a

A:Reference number: S22657; MUID:92285150

A:Accession: S22657

A:Molecule type: mRNA

A:Residues: 1-140 &lt;HIR&gt;

A:Cross-references: EMBL:X59134

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted &lt;SIG&gt;

F:20-140/Product: Ig heavy chain (fragment) #status predicted &lt;MAT&gt;

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

alignment\_scores:

Quality: 513.50 Length: 137

Ratio: 4.108 Gaps: 2

Percent Similarity: 91.241 Percent Identity: 71.533

alignment\_block:

US-09-019-441-4 x S22657 ..

Align seg 1/1 to: S22657 from: 1 to: 140

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1 ATGAGATTGGCTGAGCTGGGTTTCTTGTCTCTTTGTTGAAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa 17
51 CCAGTGTGAGTGCAGCTGTGGTGGAGTCTGGGGCGGCTTGGCAAAGCTG 100
|||||
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
101 GGGGGTCCCTGAGACTCTGTGGCGAGCCCTCCGGGTTTCAGGTTACACCTTC 150
|||||
```

```
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||
49 SerSerHisTrpMetThrTrpValArgGlnThrProGlyLysArgLeuGl 65
201 GTGGGTCTCAGCTATTAGTACTAGTGGTGATCCACATGGTACGAGACT 250
|||||
65 uTrpValAlaAsnValLysGlnAspGlySerAlaArgTyrTrpAlaAsps 82
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAAGCCAAACACACACTG 300
|||||
82 erValArgGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAspSerLeuArgAlaAspThrAlaValTyrTyrCy 115
351 TGCAGCTTGACTACAGGCTCTGACTCTGGGGCCAGGAGTCTCTGGTCA 400
|||||
115 sAlaArg...SerThrGlyIleAspTyrTrpGlyGlnGlyThrLeuValT 131
401 CCGTCTCCTCA 411
|||||
131 hrValSerSer 134
```

seq\_name: pir2:S31679

seq\_documentation\_block:

Ig heavy chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999

C:Accession: S31679

R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A:Description: Mechanisms that generate human immunoglobulin diversity operate from t

A:Reference number: S31585

A:Accession: S31679

A&gt;Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-134 &lt;CUI&gt;

A:Cross-references: EMBL:Z14203; NID:930965; PIDN:CAA78572.1; PID:930966

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology &lt;IMM&gt;

alignment\_scores:

Quality: 512.50 Length: 137

Ratio: 4.271 Gaps: 2

Percent Similarity: 87.591 Percent Identity: 74.453

alignment\_block:

US-09-019-441-4 x S31679 ..

Align seg 1/1 to: S31679 from: 1 to: 134

```
1 ATGAGTTTGGCTGAGCTGGGTTTCTCTCTCTCTTTGTTGAAAGGTGT 50
|||||
1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17
51 CCAGTGTGAGTGCAGCTGTGGTGGAGTCTGGGGCGGCTTGGCAAAGCTG 100
|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
101 GGGGGTCCCTGAGACTCTGTGGCGAGCCCTCCGGGTTTCAGGTTACACCTTC 150
|||||
34 lyArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||
49 SerSerTyrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl 65
```







OM of: U\$-09-019-441-4 to: SwissProt\_40.\* out\_format : pfs

Date: Sep 23, 2002 10:24 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:  
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-Q/cn2\_1/USPTO\_spool/US09019441/runat\_23092002\_095259\_6394/app\_query.fasta\_1.1860  
-DB=SwissProt\_40 -QFMT=fastan -SUFFIX=isp -GAPOP=12.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
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Search information block:

Query: US-09-019-441-4  
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Database: SwissProt\_40.\*  
Database sequences: 105224  
Database length: 3819550  
Search time (sec): 62.410000

score\_list:

Sequence	Strd Orig	ZScore	EScore	Len	Documentation
SwissProt_40:HV3C_HUMAN	+	494.00	855.65	4.9e-40	117   P01764 homo sapiens (human).
SwissProt_40:HV05_CARAU	+	466.50	808.13	2.2e-37	116   P19181 carassius auratus (gc
SwissProt_40:HV16_MOUSE	+	438.00	757.37	1.3e-34	136   P01783 mus musculus (mouse)
SwissProt_40:HV55_MOUSE	+	423.00	732.76	3.5e-33	117   P18526 mus musculus (mouse)
SwissProt_40:HV58_MOUSE	+	421.00	729.30	5.4e-33	117   P18529 mus musculus (mouse)
SwissProt_40:HV54_MOUSE	+	417.00	722.37	1.3e-32	117   P18525 mus musculus (mouse)
SwissProt_40:HV59_MOUSE	+	411.00	711.99	5.0e-32	117   P18534 mus musculus (mouse)
SwissProt_40:HV53_MOUSE	+	406.00	703.33	1.5e-31	117   P18524 mus musculus (mouse)
SwissProt_40:HV3A_HUMAN	+	406.00	702.96	1.5e-31	122   P01762 homo sapiens (human)
SwissProt_40:HV26_MOUSE	+	405.50	700.60	1.7e-31	144   P01795 mus musculus (mouse)
SwissProt_40:HV3T_HUMAN	+	402.00	696.48	3.7e-31	116   P01781 homo sapiens (human)
SwissProt_40:HV3E_HUMAN	+	401.00	694.91	4.6e-31	114   P01763 homo sapiens (human)
SwissProt_40:HV3G_HUMAN	+	400.00	692.57	5.8e-31	122   P01768 homo sapiens (human)
SwissProt_40:HV3J_HUMAN	+	397.50	688.32	1.0e-30	121   P01771 homo sapiens (human)
SwissProt_40:HV01_RAT	+	396.50	685.15	1.3e-30	142   P01805 rattus norvegicus (rat)
SwissProt_40:HV3H_HUMAN	+	393.00	680.45	2.7e-30	122   P01769 homo sapiens (human)
SwissProt_40:HV3E_HUMAN	+	388.50	672.81	7.4e-30	120   P01766 homo sapiens (human)
SwissProt_40:HV36_MOUSE	+	383.50	664.46	2.2e-29	116   P01806 mus musculus (mouse)
SwissProt_40:HV02_CANFA	+	382.50	662.65	2.8e-29	117   P01785 canis familiaris (dog
SwissProt_40:HV31_HUMAN	+	382.50	662.50	2.8e-29	119   P01770 homo sapiens (human)
SwissProt_40:HV32_MOUSE	+	381.50	661.08	3.5e-29	115   P01801 mus musculus (mouse)
SwissProt_40:HV3F_HUMAN	+	380.50	659.35	4.3e-29	115   P01767 homo sapiens (human)
SwissProt_40:HV3U_HUMAN	+	378.00	654.64	7.6e-29	120   P01782 homo sapiens (human)
SwissProt_40:HV3K_HUMAN	+	378.00	654.20	7.6e-29	126   P01772 homo sapiens (human)
SwissProt_40:HV3D_HUMAN	+	376.50	652.42	1.1e-28	115   P01765 homo sapiens (human)
SwissProt_40:HV27_MOUSE	+	374.50	649.12	1.6e-28	113   P01796 mus musculus (mouse)
SwissProt_40:HV30_MOUSE	+	374.50	649.12	1.6e-28	113   P01799 mus musculus (mouse)
SwissProt_40:HV29_MOUSE	+	371.50	643.93	3.2e-28	113   P01798 mus musculus (mouse)
SwissProt_40:HV31_MOUSE	+	371.50	643.93	3.2e-28	113   P01800 mus musculus (mouse)
SwissProt_40:HV03_CANFA	+	370.50	642.04	4.0e-28	115   P01802 mus musculus (mouse)
SwissProt_40:HV01_MOUSE	+	369.00	641.25	4.4e-28	114   P01784 canis familiaris (dog
SwissProt_40:HV57_MOUSE	+	369.00	640.88	5.4e-28	98   P18528 mus musculus (mouse)
SwissProt_40:HV28_MOUSE	+	368.50	638.73	6.2e-28	113   P01797 mus musculus (mouse)
SwissProt_40:HV3L_HUMAN	+	365.50	633.08	1.2e-27	119   P01773 homo sapiens (human)
SwissProt_40:HV03_CARAU	+	365.00	632.36	1.4e-27	117   P19180 carassius auratus (gc
SwissProt_40:HV20_MOUSE	+	362.00	626.80	2.7e-27	122   P01789 mus musculus (mouse)
SwissProt_40:HV18_MOUSE	+	359.50	622.39	4.6e-27	123   P01787 mus musculus (mouse)
SwissProt_40:HV21_MOUSE	+	359.50	621.60	5.2e-27	122   P01790 mus musculus (mouse)
SwissProt_40:HV56_MOUSE	+	357.50	621.06	7.0e-27	97   P18527 mus musculus (mouse)
SwissProt_40:HV34_MOUSE	+	357.50	619.69	7.1e-27	113   P01803 mus musculus (mouse)

SwissProt_40:HV37_MOUSE	+	357.00	618.36	8.0e-27	119   P01807 mus musculus (mous
SwissProt_40:HV17_MOUSE	+	356.50	617.65	8.9e-27	117   P01786 mus musculus (mous
SwissProt_40:HV23_MOUSE	+	356.50	617.20	9.0e-27	123   P01792 mus musculus (mous
SwissProt_40:HV3P_HUMAN	+	356.00	616.63	1.0e-26	119   P01777 homo sapiens (huma
SwissProt_40:HV19_MOUSE	+	355.50	615.47	1.1e-26	123   P01788 mus musculus (mous

seq\_name: SwissProt\_40:HV3C\_HUMAN

seq\_documentation\_block:

ID	HV3C_HUMAN	STANDARD;	PRT;	117 AA.
AC	P01764;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Ig heavy chain V-III region VH26 precursor.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OX	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID	9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=81101090; PubMed=6450418;			
RA	Matthysse G., Rabbitts T.H.;			
RT	"Structure and multiplicity of genes for the human immunoglobulin			
RT	heavy chain variable region.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; J00236; AAA53516.1; -			
DR	EMBL; M35415; AAA58735.1; -			
DR	PIR; A02047; H3HU26.			
DR	InterPro; IPR003006; Ig_MHC.			
DR	InterPro; IPR003596; Ig_V.			
DR	Pfam; PF00047; ig; 1.			
DR	SMART; SM00406; IGV; 1.			
KW	Immunoglobulin V region; Signal.			
FT	SIGNAL 1 19			
FT	CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.			
FT	NON_TER 117 117			
SQ	SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;			
alignment_scores:				
Quality:	494.00	Length:	118	
Ratio:	4.491	Gaps:	1	
Percent Similarity:	93.220	Percent Identity:	79.661	
alignment_block:				
US-09-019-441-4 x HV3C_HUMAN				
Align seg 1/1 to: HV3C_HUMAN from: 1 to: 117				
1 ATGAGTTTGGGCTGAGCTGGTGGTTTCTCTGCTCTTTTGAAGGTGT 50				
1 MetGluPheGlyLeuSerTrpPheLeuValalaIleLeuLysGlyVa 17				
51 CCATGTGTGAGTGCAGCTGTGGTGGAGTCTGGGGGGCGGTGGCAAGCCTG 100				
17 lglnCysgluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34				
101 GGGGGTCCCTCAGACTCTGGTGGCCAGCCTCCGGGTTTCAGGTTTACCTTC 150				
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48				
151 AATAACTACTACATGGACTGGTGGTCCGCCAGGCTCCAGGCAGGGGCTGGA 200				



```
FT CHAIN 17 136 IG HEAVY CHAIN V REGION WOPC 21.
FT DOMAIN 115 119 D SEGMENT.
FT DOMAIN 120 136 JH4 SEGMENT.
FT DISULFID 38 112
FT CONFLICT 75 78 HYAD -> DYAH (IN REF. 2).
FT CONFLICT 89 90 DN -> ND (IN REF. 2).
FT CONFLICT 115 115 W -> H (IN REF. 2).
FT CONFLICT 120 120 Y -> W (IN REF. 2).
FT NON_TER 136
SQ SEQUENCE 136 AA; 15071 MW; 2276A98DBDBF7016 CRC64;
```

```
alignment_scores:
  Quality: 438.00 Length: 137
  Ratio: 3.876 Gaps: 2
  Percent Similarity: 82.482 Percent Identity: 65.693
alignment_block:
US-09-019-441-4 x HV16_MOUSE ..
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Align seg 1/1 to: HV16\_MOUSE from: 1 to: 136

```
13 CTGAGCTGGGTTTCCTGTTCCCTTTTGAAGGTGTCCAGTGTGAGGT 62
||||| ||||||| :||||| ||||||| ||||||| |||||||
2 LeuAsnLeuValPheLeuValLeuLeuLeuGlyValGlnCysAspVa 18
63 GCAGCTGTGAGTGTGGGGCGGCTGGCAAGCCGTGGGGTCCCTGA 112
||||| ||||||| ||||||| ||||||| ||||||| |||||||
18 LcInLeuValGlySerGlyGlyLeuValGlnProGlyGlySerArgL 35
113 GACTCTGTGGCGAGCTCCGGGTTCCAGTTCACCTTCAATACTACTAC 162
:|||| ||||||| ||||||| ||||||| ||||||| |||||||
35 ysLeuSerCysAlaAlaSerGly.....PheThrPheSerSerPheGly 49
163 ATGGAGCTGGTCCCGAGGCTCCAGGCGAGGCGGTGGAGTGGTCTCAGC 212
||||| ||||||| ||||||| ||||||| ||||||| |||||||
50 MethStrpValArgGlnAlaProGluLysGlyLeuGluTrpValAlaTy 66
213 TATTAGTAGTGTGGTATCCCATGTGTACGACACTCCGTGAGGGCA 262
||||| ||||||| ||||||| ||||||| ||||||| |||||||
66 rIleSerSerGlySerThrLeuHisTyrAlaAspThrValLysGlyA 83
263 GATTCACCATCTCCAGAGAGACGCCACACACTGTTCTTCAATG 312
||||| ||||||| ||||||| ||||||| ||||||| |||||||
83 r9PheThrIleSerArgAspAsnProLysAsnThrLeuPheLeuGlnMet 99
313 AACAGCTGTAGAGTGTAGGACACGCTCTATTACTGTGCGAGCTTGAC 362
||||| ||||||| ||||||| ||||||| ||||||| |||||||
100 ThrSerLeuArgSerGluAspThrAlaMetTyrTyrCysAlaArgTrpG1 116
363 TACA.....GGGTCTGACTCTCTGGGCGAGGAGTCTGTGTC 400
:|: ||| ||||||| ||||||| ||||||| |||||||
116 yAsnTyrProTyrTyrAlaMetAspTyrTrpGlyGlnGlyThrSerValT 133
401 CCGTCTCTCA 411
133 hrValSerSer 136
```

seq\_name: SwissProt\_40:HV55\_MOUSE

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seq_documentation_block:
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 345 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=BALB/CJ;
RX MEDLINE=89279149; PubMed=2499654;
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC 1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JTO502; HVMS34.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
```

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alignment_scores:
  Quality: 423.00 Length: 118
  Ratio: 4.067 Gaps: 1
  Percent Similarity: 88.136 Percent Identity: 69.492
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alignment\_block:  
US-09-019-441-4 x HV55\_MOUSE ..

Align seg 1/1 to: HV55\_MOUSE from: 1 to: 117

```
1 ATGAGTGTGGCTGAGCTGGGTTTCTCTGCTCTCTTTTAAAGGTGT 50
||||| ||||||| :||||| ||||||| ||||||| |||||||
1 MetAsnPheGlyLeuArgLeuIlePheLeuValLeuThrLeuLysGlyVa 17
51 CCAGTGTGAGTGTGAGTGTGGAGTCTGGGGCGGTGGCAAGCCTG 100
||||| ||||||| ||||||| ||||||| ||||||| |||||||
17 lLysCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 34
101 GGGGTCTCTGAGACTCTGGTGGCGAGCTCCGGGTTCCAGTTTACCTTC 150
||||| ||||||| ||||||| ||||||| ||||||| |||||||
34 lYgLYSerLeuLysLeuSerCysAlaAlaSerGly.....PheAlaPhe 48
151 AATAACTACTACATGGACTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
:|||| ||| ||||||| ||||||| ||||||| |||||||
49 SerSerTyrAspMetSerTrpValArgGlnThrProGluLysArgLeuG1 65
201 GTGGGTCTCAGTATTAGTAGTGTGATCCACATGGTACGACAGCT 250
||||| ||||||| ||||||| ||||||| ||||||| |||||||
65 uTrpValAlaTyrIleSerSerGlyGlySerThrTyrTyrProAspT 82
251 CCGTAGGGCGAGATTCCACATCTCCAGAGAACGCCAACACACACTG 300
:|||| ||| ||||||| ||||||| ||||||| ||||||| |||||||
82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACGAGGCTGTCTATTACTG 350
:|||| ||| ||||||| ||||||| ||||||| ||||||| |||||||
99 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCy 115
351 TCGC 354
|||||
115 sAla 116
```

seq\_name: SwissProt\_40:HV58\_MOUSE

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seq_documentation_block:
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
```

DT	01-NOV-1990 (Rel. 16, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig heavy chain V region 5-76 precursor.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
OX	NCBI_TaxID=10090;
RN	[a.]
RP	SEQUENCE FROM N.A.
RC	STRAIN=BALB/CJ;
RC	MEDLINE=89279149; PubMed=2499654;
RA	Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT	"Early onset of somatic mutation in immunoglobulin VH genes during
RT	the primary immune response.";
RL	J. Exp. Med. 169:2007-2019(1989).
CC	-1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
CC	PR; JT0506; HVM557.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003596; Ig_V.
DR	Pfam: PF00047; Ig; 1.
DR	SMART: SM00406; IGV; 1.
KW	Immunoglobulin V region; Signal.
FT	SIGNAL 1 19
FT	CHAIN 20 117
FT	DOMAIN 20 49
FT	DOMAIN 50 54
FT	DOMAIN 55 68
FT	DOMAIN 69 85
FT	DOMAIN 86 117
FT	DISULFID 41 115
FT	NON_TER 117 117
SQ	SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

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alignment_scores:
    Quality: 421.00      Length: 118
    Ratio: 4.010        Gaps: 1
    Percent Similarity: 88.983   Percent Identity: 70.339

alignment_block:
    US-09-019-441-4 x HV58_MOUSE ..

Align seg 1/1 to: HV58_MOUSE from: 1 to: 117

1 ATGAGCTTGGCGTGACCTGGGTTCCTTGTTCCCTCTTTTGAAGGCTGT 50
   :::::::::::::::::::::
1 MexAsnPheValLeuSerLeuIlePheLeuAlaLeuIleLeuLysGlyVa 17
   :::::::::::::::::::::
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAAACCTG 100
   :::::::::::::::::::::
17 LGlNcYsGLuValHisLeuValGluSerGlyGlyLeuValLysProG 34
   :::::::::::::::::::::
101 GGGGGTCCCTTGACACTCTGGTGGCAGCCTCCGGGTTCAGGTTCCACTTC 150
   :::::::::::::::::::::
34 LygLySerLeuLysLeuSerCysValValSerGly.....PheThrPhe 48
   :::::::::::::::::::::
151 AATAACTACTACATGACACTGGGTGCCGCCAGGTCTCAGGCAGGGGCTGA 200
   :::::::::::::::::::::
49 AsnLySryAlaMetSerTrpValArgGlnThrProGluLysArgLeuGl 65
   :::::::::::::::::::::
201 GTGGGTCTCACGTATTAGTAGTGCTATCCCACATCGTACGCAGACT 250
   :::::::::::::::::::::
65 uIrPValAlaThrIleSerSerGlyGlyLeuTyrThrTyTrpProASP 82
   :::::::::::::::::::::
251 CCGTGAAGGCGCATTCACCATCTCCAGAGAAGGCCAACACACACTG 300
   :::::::::::::::::::::
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaGlyAsnThrLeu 98
   :::::::::::::::::::::
301 TTTCITCAATCAACAGCCTGAGACTGAGGACAGCGGTGCTATTACTG 350
   :::::::::::::::::::::
90 TyrLeuGlnMetSerSerLeuArgSerGluAspThrAlaMeTyTyTyCy 115
   :::::::::::::::::::::
351 TGGC 354

```

```

|||||
115  sala 116

seq_name: SwissProt_40:HV54_MOUSE

seq_documentation_block:
ID  HV54_MOUSE      STANDARD;      PRT;      117  AA.
AC  P18525;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1990 (Rel. 16, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  Ig heavy chain V region 5-84 precursor.
DE  Mus musculus (Mouse).
OS  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RC  SEQUENCE FROM N.A.
RC  STRAIN=BALE/CJ;
RX  MEDLINE=89279149; PubMed=2499654;
RA  Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT  "Early onset of somatic mutation in immunoglobulin VH genes during
RL  the primary immune response.";
RL  J. Exp. Med. 169:2007-2019(1989).
CC  -1- MISCELLANEOUS; THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PR  JT0505; HVMS84.
DR  InterPro: IPR003006; Ig_MHC.
DR  InterPro: IPR003596; Ig_V.
DR  Pfam: PF00047; Ig_1.
DR  SMART: SM00406; IGV; 1.
KW  Immunoglobulin V region; Signal.
FT  SIGNAL      1
FT  CHAIN       20  117
FT  DOMAIN      20  49      IG HEAVY CHAIN V REGION 5-84.
FT  DOMAIN      50  54      FRAMEWORK-1.
FT  DOMAIN      55  68      COMPLEMENTARITY-DETERMINING-1.
FT  DOMAIN      69  85      FRAMEWORK-2.
FT  DOMAIN      85  117    COMPLEMENTARITY-DETERMINING-2.
FT  DISULFID     41  115    FRAMEWORK-3.
FT  NON_TER     117  117    BY SIMILARITY.
SQ  SEQUENCE    117 AA; 12872 MW;  234055CBA469861 CRC64;

```

```

alignment_scores:
  Quality: 417.00      Length: 118
  Ratio: 3.971        Gaps: 1
  Percent Similarity: 88.983  Percent Identity: 67.797

alignment_block:
  US-09-019-441-4 x HV54_MOUSE  ..

  Align seg 1/1 to: HV54_MOUSE from: 1 to: 117

1  ATGAGAGTTTGGGCTGAGCTGGGTTTCTGTGTCCTTTTGAAGGTTG 50
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  MetAsnPheGlyLeuSerLeuIlePheLeuValLeuValLeuLysGlyVa 17

51  CCAAGTGTGAGGTCCAGCTGTGTGGAGTCTGGGGCGGCTTGGCAAGCCCTG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  lLeuCysGluValLysLeuValGluSerGlyGlyGlyLeuValGlnProG 34

101  GGGGGTCCCTGACACTCTGTGTGGCGCAGCTCCGGGTTCAGGTTACCTTC 150
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34  lyGlySerLeuLysLeuSerCysAlaAlaSerGly.....PheThrPhe 48

151  AATAACTACTACATGACTGGGTCCCGCAGGCTCCAGGGCAGGGGCTGGA 200
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49  SerSerTyrThrMetSerTrpValArgGlnThrProGluLysArgLeuCl 65

201  GTGGGTCCTCAGGTATTAGTAGTGGTGTATCCACATGGTACGCAGACT 250
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65  utrpValAlaIleSerAsnGlyGlyGlySerThrTyrTrpProAsp 82

```

SEQUENCE FROM N.A.
STRAIN=BALB/CJ;
MEDLINE=89279149; PubMed=2499654;
Levy N.S., Mallipiero U.V., Lebecque S.G., Gearhart P.J.;
"Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
J. Exp. Med. 169:2007-2019(1989).
-I- MISCCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
PR: JTO503; HVMSRF.
HSP: P01810; 2FBJ.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003596; Ig_v.
Pfam: PF00047; ig_1.
SMART: SM00406; IGv; 1.
Immunoglobulin V region; Hybridoma; Signal.
SIGNAL 1
CHAIN 19
DOMAIN 20 117
IG HEAVY CHAIN V REGION RF.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
BY SIMILARITY.
DISULFID 86 117
NON_TER 41 115
117
SEQUENCE 117 AA; 12866 MW; 2CE3295F390FF725B CRC64;

```

alignment_scores:
  Quality: 406.00      Length: 118
  Ratio: 3.942         Gaps: 1
  Percent Similarity: 87.288  Percent Identity: 66.949

alignment_block:
US-09-019-441-4 x HV53_MOUSE ..

Align seg 1/1 to: HV53_MOUSE from: 1 to: 117

1 ATCGAGCTTTGGGCTGAGCTGGGTTTTCTGTCTCTTTTGAAGGTGT 50

```

```

|||||MetAsnPheGlyLeuArgLeuValPheLeuValLeuValLeuValGlyVa 17
51 CCAGTGTGAGCTGAGCTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTC 100
| |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 lLeuCysAspValLeuValGluSerGlyGlyGlyLeuValValLeuG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GGGGTCCTCGAGACTCTGTGTCGCGAGCCTCCGGGTTCCAGGTTCCACCTTC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lYgLYSerLeuLeuSerCysAlaAlaSerGly.....PheThrPhe 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 ANTAACTACTACATGAGTGGTCCGCGCAGCTCCAGGCGAGGGGCTGGA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerTyrTyrMetSerTyrValArgGlnThrProGluLysArgLeuG 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GTGGCTTCACGATTAGTAGTGTGATCCACATGTTGATCCAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 uLeuValAlaAlaIleAsnSerAsnGlyGlySerThrTyrTyrProAsp 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 CCGTGAAGGCGAGATTCCACATCTCCAGAGAGAACGCCAACACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 hrValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 TTCTTCAATGACACCCCTGAGAGCTGAGACACGCTGTCTATTACTG 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaLeuTyrTyrCy 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TGCG 354
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
115 sAla 116

```

seq\_name: SwissProt\_40:HV3A\_HUMAN

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seq_documentation_block:
ID HV3A_HUMAN STANDARD; PRT; 122 AA.
AC P01762;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE (MYELOMA PROTEIN TRO).
RX MEDLINE=76023781; PubMed=809331;
RA Kratzin H., Altevoigt P., Ruban E., Kortt A., Starosiek K.,
RA Hilschmann N.;
RT "The primary structure of a monoclonal IgA-immunoglobulin (IgA Tro.),
RT II. The amino acid sequence of the H-chain, alpha-type, subgroup III;
RT structure of the complete IgA-molecule."
RL Hoppe-Seyler's Z. Physiol. Chem. 356:1337-1342(1975).
CC -!- MISCELLANEOUS; THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
DR PIR; A02045; ALHUTR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 1
FT NON_TER 122 122 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 122 AA; 13472 MW; 2E21A11DA04D80F9 CRC64;

```

```

alignment_scores:
  Quality: 406.00
  Ratio: 3.794
Percent Similarity: 86.290
Length: 124
Gaps: 2
Percent Identity: 60.484

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alignment\_block:

US-09-019-441-4 x HV3A\_HUMAN

Align seg 1/1 to: HV3A\_HUMAN from: 1 to: 122

```

58 GAGTCGACGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTC 107
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 GlnValGlnLeuValGlnSerGlyGlyGlyLeuValLysProGlyGlySe 17
108 CCTGAGACTCTGTGTCGCGAGCCTCCGGGTTCCAGGTTCCACCTTCAATAACT 157
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 rLeuArgLeuSerCysValAlaSerGly.....PheSerPheArgAsp 32
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
158 ACTACATGAGTGGTCCGCGCAGCTCCAGGCGAGGGCTGAGTGGGTC 207
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
32 heTyrMetSerTyrPileArg***ThrProGlyLysGlyLeu***TyrVal 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
208 TCAGTATTAGTAGTGTGATCCACATGTTGATCCAGACTCCGTCGAA 257
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerTyrIleGlySerGlySerThrLeuTyrTyrAlaAspSerVally 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
258 GGGCAGATTCCACATCTCCAGAGAGAACGCCAACACACACTGTTTCTTC 307
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 sGlyArgPheThrIleSerArgAspAsnAlaGlnLysSerLeuTyrLeu* 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
308 AATGAACACCCCTGAGAGCTGAGACACGCTGTCTATTACTGTGCGAGC 357
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 **Met***SerLeuArgThr*****ThrAlaValTyrTyrCysAlaAla 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
358 TTG.....ACTACAGGCTGCTGACTCTCGGGCCAGGG 389
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 Thr*****Phe***TyrSerThrPheSerLeu***TyrTrpGly***GI 115
| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
115 y***LeuValThrValSerSer 122

```

seq\_name: SwissProt\_40:HV26\_MOUSE

```

seq_documentation_block:
ID HV26_MOUSE STANDARD; PRT; 144 AA.
AC P01795;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region M167 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93358330; PubMed=6101208;
RA Kim S., Davis M., Sinn E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
RL Cell 27:573-581(1981).
RN [2]
RP SEQUENCE OF 20-142.
RX MEDLINE=7622762; PubMed=819932;
RA Rudikoff S., Potter M.;
RT "Size differences among immunoglobulin heavy chains from
RT phosphorylcholine-binding proteins."
RL Proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
CC -!- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM AN IGA MYELOMA PROTEIN
CC THAT BINDS PHOSPHORYLCHOLINE.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; J00516; AAC18867.1; -
DR PIR; A02071; AVMS67.

```



DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-III region WEA.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=83273707; PubMed=6410398;  
RA Gon1 F., Frangione B.;  
RT "Amino acid sequence of the Fv region of a human monoclonal IgM  
(protein WEA) with antibody activity against 3,4-pyruvylated  
galactose in Klebsiella polysaccharides K30 and K33.";  
RL Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).  
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY  
CC AGAINST 3,4-PYRUVYLATED GALACTOSE AND ISOLATED FROM A PATIENT WITH  
CC WALDENSTROM'S MACROGLOBULINEMIA.  
DR PIR; A02046; M3HUWE.  
DR HSSP; P01772; 2IG2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region.  
FT MOD\_RES 1 1  
FT NON\_TER 114 114 PYRROLIDONE CARBOXYLIC ACID.  
SQ SEQUENCE 114 AA; 12256 MW; D88294FB418A07B7 CRC64;

alignment\_scores:  
Quality: 401.00 Length: 120  
Ratio: 3.856 Gaps: 3  
Percent Similarity: 86.667 Percent Identity: 67.500

alignment\_block:

US-09-019-441-4 x HV3B\_HUMAN ..

Align seg 1/1 to: HV3B\_HUMAN from: 1 to: 114

58 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCTGGGGGTC 107  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 GlnValGlnLeuValAspSerGlyGlyLeuValGluProGlyGlySe 17  
108 CCTGAGACTCTGGTGGCGAGCTCCCGGTTCCAGGTTCCACCTTCAATAACT 157  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
17 rLeuArgLeuSerCysSerAlaSerGlyPheThrPheSerAlaAsnAsp. 33  
158 ACTACATGGAGTGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTC 207  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
34 ....MetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpLeu 48  
208 TCACGTATTAGTAGTGTGTGATCCACATGTGTACGACACATCCCGTAA 257  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
49 SerPheIleGlySerGlySerThrIleTyrTrpAlaAspSerVally 65  
258 GGCAGATTACCATCTCCAGAGAGACGCGCAACACACTGTTCTTC 307  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
65 sGlyArgPheThrIleSerArgAsn\*\*\*SerLysAsnSerLeuTyrLeuG 82  
308 AATGAACACCTGAGAGCTGAGACACAGGCTGTCTATTACTGTGGAGC 357  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
82 InMetSerSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98  
358 .....TTGACTACAGGCTGACTCTCTGGGGCGAGGAGTCTGTGCTAC 401  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
99 GlyTrpLeuLeu.....AsnTrpGlyGlnGlyThrLeuValTh 111  
402 CGTCTCTCA 411  
|||||:|||||  
111 rValSerSer 114

seq\_name: SwissProt\_40:HV3G\_HUMAN

seq\_documentation\_block:  
AC HV3G\_HUMAN STANDARD; PRT; 122 AA.  
ID P01768;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig heavy chain V-III region CAM.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81013859; PubMed=6774332;  
RA Lehman D.W., Putnam F.W.;  
RT "Amino acid sequence of the variable region of a human mu chain:  
RT location of a possible JH segment.";  
RL Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980).  
CC -1- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A  
CC PATIENT WITH MACROGLOBULINEMIA.  
DR PIR; A02051; M3HUAM.  
DR HSSP; P01772; 2IG2.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig\_1.  
DR SMART; SM00406; IgV; 1.  
KW Immunoglobulin V region.  
FT MOD\_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.  
FT NON\_TER 122 122  
SQ SEQUENCE 122 AA; 13668 MW; A42D0F17D252F1C2 CRC64;

alignment\_scores:  
Quality: 400.00 Length: 124  
Ratio: 3.922 Gaps: 2  
Percent Similarity: 82.258 Percent Identity: 63.710

alignment\_block:

US-09-019-441-4 x HV3G\_HUMAN ..

Align seg 1/1 to: HV3G\_HUMAN from: 1 to: 122

58 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCTGGGGGTC 107  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
1 GlnValGlnLeuValGluSerGlyGlyValVal\*\*\*ProGlyArgSe 17  
108 CCTGAGACTCTGGTGGCGAGCTCCCGGTTCCAGGTTCCACCTTCAATAACT 157  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
17 rLeuArgLeuSerCysAlaAlaSerGly.....PheThrPheSerAsnT 32  
158 ACTACATGGAGTGGTCCGCCAGGCTCCAGGCGAGGGCTGGAGTGGGTC 207  
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
32 yrAlaMetHisTrpValArgGlnProGlyLysGlyLeuGluTrpVal 48  
208 TCACGTATTAGTAGTGTGTGATCCACATGTGTACGACACATCCCGTAA 257  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
49 AlaValIleSerTyr\*\*\*Gly\*\*\*Lys\*\*\*Lys\*\*\*Lys\*\*\*SerVally 65  
258 GGCAGATTACCATCTCCAGAGAGACGCGCAACACACTGTTCTTC 307  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
65 sGlyArgPheThrIleSerArgAsp\*\*\*SerLys\*\*\*ThrLeuTyrLeuG 82  
308 AATGAACACCTGAGAGCTGAGACACAGGCTGTCTATTACTGTGCG... 354  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
82 InMetAsnSerLeuArgAlaGlu\*\*\*ThrAlaValTyrTyrCysAlaArg 98  
355 .....AGCTTGACTACAGGCTGACTCTCTGGGGCGAGG 389  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
99 AspArgProLeuTyrGly\*\*\*TyrArgAlaPheAsnTyrTrpGlyGlnI 115  
390 AGTCTGTGTCACCGTCTCTCTCA 411  
|||||:|||||  
115 yThrLeuValThrValSerSer 122





```
295  A C A C T G T T T C T T C A A A T G A C A G C C T G A G A C C T G A G G A C A C G G C T G T C T A 344
      :::::|||||
99   I l e V a l T y r L e u G l n M e t A s n I l e A r g S e r G l u A s p T h r G l y I l e T y 115
      :::::|||||
345  T T A C T G T C G A G C T T G A C T A C A G G G T C T G A C T C C . . . . . T 379
      |||||:::
115  r T y r C y s S e r A r g G l y T y r G l y T y r S e r G l u A s n T r p P h e V a l T y r T 132
      |||||:::
380  G G G C C C A G G G A G T C C T G G T C A C C G T C T C C T C A 411
      |||||:::
132  r p G l y G l n G l y T h r L e u V a l T h r V a l S e r S e r 142
```

Sequence	Strd Orig	ZScore	EScore	Len	Documentation	...
sp_human:Q96BB9	+	532.50	1012.41	8.0e-49	597	Q96bb9 homo sapiens (human).
sp_human:Q96K68	+	503.00	956.98	1.2e-45	494	Q96k68 homo sapiens (human).
sp_rotent:Q99KA4	+	465.00	883.42	1.5e-41	487	Q99ka4 mus musculus (mouse).
sp_rotent:Q91Z05	+	455.00	864.30	1.8e-40	473	Q91z05 mus musculus (mouse).
sp_rotent:Q91WP5	+	449.50	853.91	7.1e-40	479	Q91wp5 mus musculus (mouse).
sp_rotent:Q91XE1	+	442.50	839.92	4.1e-39	480	Q91xe1 mus musculus (mouse).
sp_human:Q9UL71	+	437.50	843.23	1.1e-38	121	Q9ul71 homo sapiens (human).
sp_rotent:Q91Z07	+	434.50	824.28	3.0e-38	486	Q91z07 mus musculus (mouse).
sp_human:Q9UL91	+	429.00	826.98	8.7e-38	118	Q9ul91 homo sapiens (human).
sp_rotent:Q9HCC1	+	423.00	815.84	3.8e-37	112	Q9hcc1 homo sapiens (human).
sp_human:Q9UL90	+	421.50	812.84	5.6e-37	113	Q9ul90 homo sapiens (human).
sp_human:Q9UL84	+	412.00	793.70	6.0e-36	122	Q9ul84 homo sapiens (human).
sp_human:Q9UL93	+	410.50	791.26	8.6e-36	116	Q9ul93 homo sapiens (human).
sp_human:Q9UL72	+	410.00	790.13	9.6e-36	118	Q9ul72 homo sapiens (human).
sp_rotent:Q920E7	+	401.50	773.57	8.1e-35	119	Q920e7 mus musculus (mouse).
sp_human:Q9UL88	+	394.50	759.08	4.7e-34	131	Q9ul88 homo sapiens (human).
sp_human:Q9Y509	+	393.00	755.09	1.0e-34	147	Q9y509 homo sapiens (human).
sp_human:Q9ULB6	+	380.00	733.99	1.6e-32	95	Q9ulb6 homo sapiens (human).
sp_rotent:Q9QYF0	+	352.00	668.90	2.2e-29	298	Q9qyf0 mus musculus (mouse).
sp_human:Q9UL92	+	344.00	661.66	1.9e-28	124	Q9ul92 homo sapiens (human).
sp_human:Q9UGP3	+	342.50	659.71	1.9e-28	112	Q9ugp3 homo sapiens (human).
sp_rotent:Q9R1A4	+	340.00	642.01	4.7e-28	437	Q9r1a4 mus musculus (mouse).
sp_rotent:Q9DBL4	+	339.50	640.29	4.5e-28	473	Q9db14 mus musculus (mouse).
sp_human:Q9UL87	+	334.50	644.89	1.4e-27	104	Q9ul87 homo sapiens (human).
sp_human:Q9QSO0	+	327.00	626.34	9.6e-27	159	Q9qso0 homo sapiens (human).
sp_human:Q9UL95	+	324.50	623.76	1.7e-26	125	Q9ul95 homo sapiens (human).
sp_rotent:Q9N0W6	+	322.00	618.97	3.2e-26	124	Q9n0w4 oryctolagus cuniculus (rabbit).
sp_mammal:Q9N0M6	+	319.00	613.17	6.7e-26	124	Q9n0w6 oryctolagus cuniculus (rabbit).
sp_human:Q9UL94	+	310.50	597.08	5.5e-25	119	Q9ul94 homo sapiens (human).
sp_rotent:Q9L9A6	+	308.50	579.95	1.2e-24	484	Q9l9a6 mus musculus (mouse).
sp_human:Q9BRV0	+	308.00	578.67	1.4e-24	500	Q9brv0 homo sapiens (human).
sp_rotent:Q91WT1	+	307.50	578.07	1.6e-24	481	Q91wt1 mus musculus (mouse).
sp_human:Q9EGA6	+	302.50	566.07	5.7e-24	614	Q9ega6 homo sapiens (human).
sp_rotent:Q924P9	+	301.00	576.92	6.1e-24	143	Q924p9 mus musculus (mouse).
sp_rotent:Q9L3L1	+	300.50	564.75	8.8e-24	468	Q9l3l1 mus musculus (mouse).
sp_rotent:Q9L1C4	+	300.00	563.88	1.0e-23	463	Q9l1c4 mus musculus (mouse).
sp_rotent:Q92M22	+	296.50	556.78	2.4e-23	479	Q92m22 mus musculus (mouse).
sp_rotent:Q924R2	+	295.50	566.45	2.4e-23	140	Q924r2 mus musculus (mouse).
sp_rotent:Q921A6	+	295.00	567.09	2.6e-23	118	Q921a6 mus musculus (mouse).
sp_rotent:Q921A5	+	295.00	560.35	3.0e-23	241	Q921a5 mus musculus (mouse).

132 spTyrTrpGlyGlnGlyThrLeuValThrValSerSer 144

seq\_name: sp\_human:Q96K68

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seq_documentation_block:
ID Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE CDNA FLJ14473 F15, CLONE MAMMAL1001080, HIGHLY SIMILAR TO HOMO
DE SAPIENS SNC73 PROTEIN (SNC73) MRNA.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Watanabe S., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yanamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Nanamiya K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK027379; BAB55072.1;
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AEB5AE4C0E CRC64;

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alignment\_scores:

Quality: 503.00 Length: 143  
Ratio: 4.123 Gaps: 2  
Percent Similarity: 85.315 Percent Identity: 69.930

alignment\_block:

US-09-019-441-4 x Q96K68 ..

Align seg 1/1 to: Q96K68 from: 1 to: 494

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1 ATGGAGTTTGGGCTGAGCTGGTTCCTTCTGCTCTTTTGAAGGTGT 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetGluLeuGlyLeuArgTrpValPheLeuValAlaPheLeuGluGly 17

51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 LGlnCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGGCAGCCTCCGGGTTTCAGGTTTCACCTTC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LGlySerLeuArgLeuSerCysAlaAlaSerGly.....LeuSerPhe 48

151 AATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGGCAGGGGTGGA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerThrTyrAlaMetAsnTrpValArgGlnAlaProGlyLysGlyLeuG 65

201 GTGGGTCTCAGTATTAGTAGTGTGATCCACATGTCAGTCAGCAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 utrpValSerSerIleSerSerArgSerAspTyrIleTyrTrpArgAsp 82

251 CCGTGAAGGCAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98

301 TTCTTCAATGACACCGCTGAGAGTGGACACCGCTGTCTATTACTG 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TyrLeuGlnMetAsnSerLeuArgValArgValAspThrAlaValTyrTrp 115

351 TGCG.....AGCTTGACTACAGGCTCTGACTCTCGG 382
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
115 sAlaArgAspSerCysAsnGlyAlaIleCysTyrGlyPheSerProTrpG 132

```

383 GCCAGGGAGTCTGCTACCTGCTCTCTCTCA 411  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
132 lyGlnGlyThrLeuValThrValSerSer 141

seq\_name: sp\_rodent:Q99KA4

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seq_documentation_block:
ID Q99KA4 PRELIMINARY; PRT; 487 AA.
AC Q99KA4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HPOTHEICAL 52.6 KDA PROTEIN.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004786; AAH04786.1;
DR HSP: P01810; 2FBJ
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_4.
DR SMART: SM00409; IG; 3.
DR SMART: SM00407; IGcl; 3.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00410; IG_like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein
SQ SEQUENCE 487 AA; 52554 MW; 7DC9E96DB333077B CRC64;

```

alignment\_scores:

Quality: 465.00 Length: 145  
Ratio: 3.908 Gaps: 2  
Percent Similarity: 82.069 Percent Identity: 64.138

alignment\_block:

US-09-019-441-4 x Q99KA4 ..

Align seg 1/1 to: Q99KA4 from: 1 to: 487

```

1 ATGGAGTTTGGGCTGAGCTGGTTCCTTCTGCTCTTTTGAAGGTGT 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetAsnPheGlyLeuSerLeuIlePheLeuValLeuValLysGly 17

51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 LGlnCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 34

101 GGGGGTCCCTGAGACTCTGGTGGCAGCCTCCGGGTTTCAGGTTTCACCTTC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 LGlySerLeuLysLeuSerCysAlaAlaSerGly.....PheThrPhe 48

151 AATAACTACTACATGAGTGGTCCGCCAGGCTCCAGGGCAGGGGTGGA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerTyrAlaMetSerTrpValArgGlnThrProGlyLysArgLeuG 65

201 GTGGGTCTCAGTATTAGTAGTGTGATCCACATGTCAGTCAGCAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 utrpValAlaThrIleSerAspGlySerTyrThrTyrTrpAsp 82

251 CCCTGAAGGCAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 snValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnLeu 98

```



|||||  
129 laValThrValSerSer 134

seq\_name: sp\_rodent:Q91XE1

seq\_documentation\_block:  
ID Q91XE1 PRELIMINARY; PRT; 480 AA.  
AC Q91XE1;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE UNKNOWN (PROTEIN FOR IMAGE:4224494) (FRAGMENT).  
OS Mus musculus (Mouse)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC010798; AAH10798.1; -;  
FT NON\_TER 1  
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

alignment\_scores:  
Quality: 442.50 Length: 139  
Ratio: 3.916 Gaps: 3  
Percent Similarity: 81.295 Percent Identity: 66.187

alignment\_block:

US-09-019-441-4 x Q91XE1 ..

Align seg 1/1 to: Q91XE1 from: 1 to: 480

7 TTTGGCTGAGTGGGTTTCTCTTTGAAAGGTGCCAGTG 56  
|||||  
2 PheGlyLeuSerLeuIlePheLeuValLeuIleLeuLysGlyValLeuCy 18  
|||||  
57 TGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGT 106  
|||||  
18 sAspValLysLeuValGluSerGlyGlyLeuValLysProGlyGlys 35  
|||||  
107 CCTGACACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTCAATAAC 156  
|||||  
35 erLeuArgLeuSerCysAlaAlaSerGly.....PheIlePheSerAsn 49  
|||||  
157 TACTACATGGACTGGGTCCGCCAGGCTCCAGGGCGGTGGAGTGGGT 206  
|||||  
50 SerTyrMetSerTrpValArgGlnThrProGluLysArgLeuGluTrpVa 66  
|||||  
207 CTCACGTATTAGTAGTGGTGGATCCCATGTCAGCAGACTCCGTGA 256  
|||||  
66 lAlaThrIleSerAsnSerGlyTyrAlaThrHisTyrProAspSerMetL 83  
|||||  
257 AGGCAGATTCCACATCTCCAGAGAGNACCCACACACACTGTTCTT 306  
|||||  
83 ySgLyArgPheThrIleSerArgAspAsnAlaGlnAsnThrValLeu 99  
|||||  
307 CAATGAACACCGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGGAG 356  
|||||  
100 GlnMetThrSerLeuAsnSerGluAspThrAlaValTyrTyrCys..... 114  
|||||  
357 CTGACTACAGGTCT.....GACTCCTGGGGCCAGGAGTGCC 394  
|||||  
115 ....ThrArgGlyAspTyrTrpTyrPheAspValTrpGlyAlaGlyThr 130  
|||||  
395 TGGTCCCGTCTCTCA 411  
|||||  
136 hrValThrValSerSer 135  
|||||  
seq\_name: sp\_human:Q9UL71

seq\_documentation\_block:

ID Q9UL71 PRELIMINARY; PRT; 121 AA.  
AC Q9UL71;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=9877739; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035043; AAD56279.1; -;  
DR HSSP; P01772; 2FB4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 121  
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

alignment\_scores:

Quality: 437.50 Length: 123  
Ratio: 4.051 Gaps: 3  
Percent Similarity: 87.805 Percent Identity: 71.545

alignment\_block:

US-09-019-441-4 x Q9UL71 ..

Align seg 1/1 to: Q9UL71 from: 1 to: 121

58 GAGGTCCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTGGGGGTG 107  
|||||  
1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlyGlySe 17  
|||||  
108 CCTGAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTCAATAACT 157  
|||||  
17 rLeuArgLeuPheCysAlaAlaSerGly.....PheThrPheAspGlyT 32  
|||||  
158 ACTACATGGACTGGTCCGCCAGGCTCCAGGCGAGGCTGGAGTGGGTG 207  
|||||  
32 yrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48  
|||||  
208 TCACGTATTAGTAGTGGTGGATCCCATGTCAGCAGACTCCGTGAA 257  
|||||  
49 SerLeuIleSerGlyAspGlyGlySerThrTyrTyrAlaAspSerVal 65  
|||||  
258 GGCAGATTCCACCATCTCCAGAGAACGCCAACACACTGTCTTCTTC 307  
|||||  
65 sGlyArgPheThrIleSerArgAspAsnSerLysAsnSerLeuTyrLeuG 82  
|||||  
308 AATGAACACCGCTGAGAGCTGAGGACACCGCTGTCTATTACTGTGG... 354  
|||||  
82 lnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrTyrCysAlaLys 98  
|||||  
355 ...AGCTTGACTACA.....GGTCTGACTCTCTGGGGCCAGGAGT 392  
|||||  
99 GlyLysValThrThrIleTyrAspArgPheAspIleTrpGlyGlnGlyTh 115  
|||||  
393 CCTGGTCCAGCTCTCTCA 411  
|||||  
115 rMetValThrValSerSer 121

seq\_name: sp\_rodent:Q91207

seq\_documentation\_block:

ID Q91207 PRELIMINARY; PRT; 486 AA.  
 AC Q91207;  
 DT 01-DEC-2001 (Tremblrel. 19, Created)  
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE HYPOTHETICAL 52.7 KDA PROTEIN.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC010324; AAH10324.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 486 AA; 52682 MW; 4FEF835125DA870B CRC64;

alignment\_scores:  
 Quality: 434.50 Length: 145  
 Ratio: 3.682 Gaps: 4  
 Percent Similarity: 81.379 Percent Identity: 61.379

alignment\_block:

US-09-019-441-4 x Q91207 ..

Align seg 1/1 to: Q91207 from: 1 to: 486

1 ATGAGTTGGCTGAGCTGGTTCCTTTCTCTTTTGAAGGTGT 50  
 |||:||||| |||:||||| |||:||||| |||:|||||  
 1 MetAsnPheGlyLeuArgLeuIlePheLeuValLeuAlaLeuLysGlyVa 17  
 51 CCAGTGTGAGTCCAGCTGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 17 lGnCysGluValHisLeuValGluSerGlyGlyLeuValLysProG 34  
 101 GGGGGTCCCTGAGACTGTGTGGCGGAGCTCCGGGTTTCAGGTTACCTTC 150  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 34 lYgLySerLeuLysLeuSerCysValValSerGlyPheSerPheThr... 49  
 151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGGTGGA 200  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 50 ...SerTyrAspMetSerTrpValArgGlnThrProGluArgArgLeuG 65  
 201 GTGGGCTCAGCTATTAGTAGTAGTGGTATCCACATGTCAGCAGACT 250  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 65 utrPvalAlaAlaIleThrSerGlyGlyAsn...ThrTyrTyrProAspA 81  
 251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 81 snValLysGlyArgPheThrValSerArgAspAlaLysTyrThrLeu 97  
 301 TTTCTTCAATGAACGCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 98 TyrLeuGlnMetSerSerLeuLysSerGluAspThrAlaMetTyrTyrCy 114  
 351 TGGGAGC.....TTGACTACAGGGTCT.....GACT 376  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 114 svalArgProGluIleProIleTyrTyrTyrSerGlySerTyrPheAsps 131  
 377 CTGGGGCCAGGAGCTCCTGGTCCACGCTCCCTCA 411  
 131 entrrpGlyGlnGlyThrThrIleThrValSerSer 142

seq\_name: sp\_human:Q9UL91

seq\_documentation\_block:

ID, Q9UL91 PRELIMINARY; PRT; 118 AA.

AC Q9UL91;  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=98277139; PubMed=9614934;  
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
 RA Young D.C.;  
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus";  
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
 DR EMBL; AF035023; AAD56259.1; -;  
 DR HSP; P01772; 2FB4.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; Igv; 1.  
 FT NON\_TER 1  
 FT NON\_TER 118 118  
 SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

alignment\_scores:  
 Quality: 429.00 Length: 119  
 Ratio: 4.125 Gaps: 2  
 Percent Similarity: 87.395 Percent Identity: 73.109

alignment\_block:

US-09-019-441-4 x Q9UL91 ..

Align seg 1/1 to: Q9UL91 from: 1 to: 118

58 GAGGTGCAGCTGTGTGAGTCTGGGGCGGCTTGGCAAAGCTGGGGGTC 107  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlyse 17  
 108 CTGAGACTCTGTGGCGCAGCTCCGGGTTTCAGGTTCACTCAATAACT 157  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 17 rLeuArgLeuSerCysAlaAlaSerGly.....PheThrPheSerSert 32  
 158 ACTACATGGAGTGGTCCGCCAGGCTCCAGGCGAGGGGTGGAGTGGGTC 207  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 32 yrSerMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48  
 208 TCACGTATTAGTAGTGTGTATCCACATGGTACGACACTCCGCTGAA 257  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 49 SerTyrIleSerSerThrIleIleThrIleTyrTyrAlaAspSerVally 65  
 258 GGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTGTTCTTC 307  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuG 82  
 308 AATGAACAGCCTGAGAGCTGAGGACACAGGCTGTCTATTACTGTGCG... 354  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 82 lntMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98  
 355 ...AGCTTGACTACAGGCTGTGACTCCTCTGGGGCAGGGAGTCTGGTTCAC 401  
 |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||  
 99 GlyAspSerSerGluAlaPheAspIleTrpGlyGlnGlyThrMetValTh 115  
 402 CGTCTCC 408  
 |||:|||||  
 115 rValSer 117

seq\_name: sp\_human:Q9HCC1

```
seq_documentation_block:
ID Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT).
DE Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RT "An antibody fragmentA3 specific for native lysozyme: Isolaion from a
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB049915; BAB16829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_Like; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24F1A45EC3B84788 CRC64;

alignment_scores:
Quality: 423.00 Length: 114
Ratio: 4.273 Gaps: 1
Percent Similarity: 86.842 Percent Identity: 72.807

alignment_block:
US-09-019-441-4 x Q9HCC1 ..
Align seg 1/1 to: Q9HCC1 from: 1 to: 112

58 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCGCTGGGGGTC 107
|||||
1 GluValGlnLeuValGluSerGlyGlyValValArgProGlyGlyse 17
108 CCTGAGACTCTGGTGGCGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACT 157
|||||
17 rLeuArgIleSerCysAlaAlaSerGly.....PheThrPheAspAspt 32
158 ACTACATGGAGTGGTCCGCGCAGGCTCCAGGCGAGGGCTGGAGTGGGTC 207
|||
32 YrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48
208 TCAGTATTAGTAGTAGTGGTGATCCACATGGTACGACAGCTCCGTGAA 257
|||
49 SerGlyIleAsnTrpAsnGlyGlySerThrGlyTyrAlaAspSerVally 65
258 GGCAGATTACCATCTCCAGAGAGACGCCACACACACTGTTCTTC 307
|||||
65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeuTyrLeuG 82
308 AAATGAACAGCTGAGAGCTGAGGACAGCGGCTGCTATTACTGTGGAGC 357
|||||
82 InMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaArg 98
358 TTGACTACAGGCTGACTCTCGGGCGGCGAGGAGTCTGTGTC 399
|||
99 ArgArgTyrAlaLeuAspTyrTrpGlyGlnGlyThrLeuVal 112

seq_name: sp_human:Q9UL90
seq_documentation_block:
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ID Q9UL90 PRELIMINARY; PRT; 113 AA.
AC
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

alignment_scores:
Quality: 421.50 Length: 118
Ratio: 4.132 Gaps: 2
Percent Similarity: 86.441 Percent Identity: 72.034

alignment_block:
US-09-019-441-4 x Q9UL90 ..
Align seg 1/1 to: Q9UL90 from: 1 to: 113

58 GAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCGCTGGGGGTC 107
|||||
1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlyGlyse 17
108 CCTGAGACTCTGGTGGCGCAGCCTCCGGGTTTCAGGTTTCACCTTCAATAACT 157
|||||
17 rLeuArgLeuSerCysAlaAlaSerGly.....PheThrPheSerSert 32
158 ACTACATGGAGTGGTCCGCGCAGGCTCCAGGCGAGGGCTGGAGTGGGTC 207
|||
32 YrGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48
208 TCAGTATTAGTAGTAGTGGTGATCCACATGGTACGACAGCTCCGTGAA 257
|||
49 AlaPheIleArgTyrAspGlySerAsnLysTyrTyrAlaAspSerVally 65
258 GGCAGATTACCATCTCCAGAGAGAACGCCAACACACTGTTCTTC 307
|||||
65 sGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrLeuG 82
308 AAATGAACAGCTGAGAGCTGAGGACAGCGGCTGCTATTACTGTGGAGC 357
|||||
82 InMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCysAlaLys 98
358 TTGACTACAGGCTGACTCTCGGGCGGCGAGGAGTCTGTGTCACCGCTCTC 407
|||
99 .....AspLeuAsnTyrTrpGlyGlnGlyThrLeuValThrValse 112
408 CTCA 411
112 rSer 113

seq_name: sp_human:Q9UL84
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seq_documentation_block:
ID Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

alignment_scores:
Quality: 412.00 Length: 124
Ratio: 4.039 Gaps: 2
Percent Similarity: 82.258 Percent Identity: 68.548

alignment_block:
US-09-019-441-4 x Q9UL84
Align seg 1/1 to: Q9UL84 from: 1 to: 122

58 GAGGTGCGAGCTGTGGAGTCTGGGGCGGCTTGGCAAAGCTGGGGGTC 107
|||||
1 GluValGlnLeuValGluSerGlyGlyValValGlnProGlyArgSe 17
108 CTGAGACTCTGGGCGCAGCCTCCGGGTCAGGTTCCACCTTCAATAACT 157
|||||
17 rLeuArgLeuSerCysAlaAlaSer.....ArgPheThrPheSerAsnT 32
158 ACTACATGGAGTGGTCCCGCAGGCTCCAGGCGAGGGCTGGAGTGGTC 207
|||||
32 yGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpVal 48
208 TCAGTATTAGTACTGTGTGATCCACATGTGTACGAGACTCCGTCAA 257
::: |||||:::
49 AlaAlaIleSerAsnAspGlySerAsnLysPheTyrrAlaAspSerVally 65
258 GGGCAGATTACCATCTCCAGAGAGACGGCCACACACACTGTTTCTTC 307
|||||
65 sGlyArgPheThrIlePheArgAspAsnSerLysAsnMetMetAspLeuG 82
308 AAATGACACGCTCAGAGCTCAGACACGGCTGTCTATTACTGTCCGAGC 357
|||||
82 InMetAsnSerLeuArgAlaGluAspThrAlaValTyrrCysAlaLys 98
358 .....TTGACTACAGGCTCTGACTCTCTGGGGCCAGGG 389
::: ||| ||| |||||
99 AspGluArgGlyArgLeuValGlyThyTyrrPheAspTyrrTrpGlyGlnG 115
390 AGTCCTGGTCACCGTCTCTCTCA 411
|||||
115 yThrLeuValThrValSerSer 122
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```
seq_name: sp_human:Q9UL93
seq_documentation_block:
ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSP; P01772; 2FBA.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

alignment_scores:
Quality: 410.50 Length: 118
Ratio: 4.064 Gaps: 2
Percent Similarity: 85.593 Percent Identity: 71.186

alignment_block:
US-09-019-441-4 x Q9UL93
Align seg 1/1 to: Q9UL93 from: 1 to: 116

61 GTGAGCTGTGGAGTCTGGGGCGGCTTGGCAAAGCTGGGGGTCCT 110
|||||
1 ValGlnLeuValGluSerGlyGlyValValGlnProGlyArgSerLe 17
111 GAGACTCTGTGCGCAGCTCCGGGTTTCAGGTTCCACCTTCAATAACTACT 160
|||||
17 uArgLeuSerCysAlaAlaSerGly.....PheThrPheSerSerTyra 32
161 ACATGGAGTGGTCCCGCAGGCTCCAGGCGAGGGCTGGAGTGGTCTCA 210
|||||
32 laMetHisTrpValArgGlnAlaProGlyLysGlyLeuGluTrpValala 48
211 CGTATTAGTACTGTGTGATCCACATGTGTACGAGACTCCGTCAAGGG 260
|||||
49 ValIleSerTyrrAspGlySerAsnLysTyrrAlaAspSerVallySGl 65
261 CAGATTCCACATCTCCAGAGAGAACGCCAACACACACTGTCTTCTCAA 310
|||||
65 yArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyrrLeuGlnM 82
311 TGAACAGCCTGAGAGCTCAGGACACGGCTGTCTATTACTGTGCG...AGC 357
|||||
82 etAsnSerLeuArgAlaGluAspThrAlaMetTyrrCysAlaGlyGly 98
358 TTGACTACAGGCTCTGACTCCTGGGGCCAGGAGTCTGTGTCACCGTCTC 407
|||||
99 GlyGlyLeuGlyLeuGlyTyrrTrpGlyGlnGlyThrLeuValThrValse 115
408 CTCA 411
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||||  
115 rSer 116

seq\_name: sp\_human:Q9UL72

seq\_documentation\_block:  
ID Q9UL72 PRELIMINARY; PRT; 118 AA.

AC Q9UL72;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL: AF035042; AD56278.1; -;  
DR HSSP: P01772; 2FB4.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
FT NON\_TER 1  
FT NON\_TER 118  
SQ SEQUENCE 118 AA; 12872 MW; B4DIA5944B2D5CCA CRC64;

alignment\_scores:  
Quality: 410.00 Length: 121  
Ratio: 4.020 Gaps: 3  
Percent Similarity: 84.298 Percent Identity: 71.074

alignment\_block:

US-09-019-441-4 x Q9UL72 ..

Align seg 1/1 to: Q9UL72 from: 1 to: 118

58 GAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAAGCGCTGGGGGTC 107  
|||||  
1 GluValGlnLeuValGluSerGlyGlyLeuValGlnProGlyGlySe 17  
108 CCTGAGACTCTGGTGGCCAGCTCCCGGGTTCAGGTTACCTTCAATAACT 157  
|||||  
17 rLeuArgLeuSerCysAlaAlaSerGly.....PheThrValSerSerA 32  
158 ACTACATGAGTGGTCCGCCAGCTCCAGGCGAGGCGCTGGAGTGGGTC 207  
|||||  
32 snTyMetAsnTrpValArgGlnAlaProGlyLysGlyLeuGluSerVal 48  
208 TCAGCTATTAGTAGTGGTGTGATCCCATGTTACGACACTCCCGTAA 257  
|||||  
49 Ser...ValThrTySerGlyGlySerSerTyTyTyAlaAspSerVally 64  
258 GGCAGATTACCATCTCCAGAGAGAACGCCAACACACTGTTTCTTC 307  
|||||  
64 sGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeuTyTyLeuG 81  
308 AAATGAACACCTTCAGAGCTGAGGACACGCTGCTATTACTGTGGAGC 357  
|||||  
81 InMetAsnSerLeuArgAlaGluAspThrAlaPheTyTyTyCysAlaArg 97  
358 TTGACTACAGGTCT.....GACTCTGGGGCCAGGAGTCTCTGGT 398  
|||||  
98 AspArgPheGlyGluPheLeuPheAspTyTrpGlyGlnGlyThrLeuVa 114

399 CACCGTCTCCTCA 411  
|||||  
114 lThrValSerSer 118

seq\_name: sp\_rodent:Q920E7

seq\_documentation\_block:

ID Q920E7 PRELIMINARY; PRT; 119 AA.  
AC Q920E7;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PTERIN-MIMICKING ANTI-IDIOCOPE HEAVY CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Atkin J.D., Iape A., Jennings I.G., Horaitis O., Cotton R.G.H.;  
RT "Definition of the Idiotope of Pterin-Mimicking Antibodies Expressed  
RT in Mammalian Cells.";  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF307937; AAL09421.1; -;  
FT NON\_TER 1  
FT NON\_TER 119  
SQ SEQUENCE 119 AA; 13025 MW; F6E904044381CA7C CRC64;

alignment\_scores:

Quality: 401.50 Length: 121  
Ratio: 3.898 Gaps: 2  
Percent Similarity: 85.124 Percent Identity: 66.942

alignment\_block:

US-09-019-441-4 x Q920E7 ..

Align seg 1/1 to: Q920E7 from: 1 to: 119

58 GAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAAGCGCTGGGGGTC 107  
|||||  
1 GluValGlnLeuValGluSerGlyGlyAspLeuValLysProGlyGlySe 17  
108 CCTGAGACTCTGGTGGCCAGCTCCCGGGTTCAGGTTACCTTCAATAACT 157  
|||||  
17 rLeuLysLeuSerCysAlaAlaSerGly.....PheThrPheSerSerT 32  
158 ACTACATGAGTGGTCCGCCAGCTCCAGGCGAGGCGCTGGAGTGGGTC 207  
|||||  
32 yrGlyMetSerTrpValArgGlnThrProAspLysArgLeuGluTrpVal 48  
208 TCAGCTATTAGTAGTGGTGTGATCCCATGTTACGACACTCCCGTAA 257  
|||||  
49 AlaThrIleSerSerGlyGlySerTyTyTyTrpProAspSerVally 65  
258 GGCAGATTACCATCTCCAGAGAACGCCAACACACTGTTTCTTC 307  
|||||  
65 sGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeuTyTyLeuG 82  
308 AAATGAACACCTTCAGAGCTGAGGACACGCTGCTATTACTGTGCG... 354  
|||||  
82 InMetSerSerLeuLysSerGluAspThrAlaMetTyTyTyCysAlaArg 98  
355 .....AGCTTGACTACAGGTCTGACTCTCTGGGGCCAGGAGTCTCTGGT 398  
|||||  
99 HisGlyAspTyTrpAspValGlyPheAlaTyTrpGlyGlnGlyThrLeuVa 115  
399 CACCGTCTCCTCA 411  
|||||  
115 lThrValSerAla 119



1 ATGAGATTGGCGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTG 50  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17  
51 CCAGTGTGAGGTGCAGCTGCTGGAGTCTGGGGGGCGCTTGGCAAAGCTG 100  
17 lGncysgluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTCTGCTGGCGCAGCCFCCGGGTTCAAGTTCACCTTC 150  
34 lYglySerLeuArgLeuSerCysAlaAlaSerGly.....PheTrpPhe 48  
151 AATAACTACTACATGAGACTGGGTCGCCAGGCTCCAGGCAGGGCGCTGA 200  
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65  
201 GTGGGTCTACGCTATTAGTAGTAGTGGTGATCCCATGGTACGCAGACT 250  
65 utrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAspS 82  
251 CCGTGAAGGCGAGATTCCACTCTCCAGAGAGNACGCCAACACACACTG 300  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGTCTATTACTG 350  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115  
351 TCGGAGC.....TTGACTACAGGCTCTG 373  
115 salalysGlyTyrSerSerGlyTrpTyrTyrTyrTyrTyrTyrGlyMetA 132  
374 ACTCTCTGGGCCAGGAGTCCCTGGTCAACGCTCTCTCA 411  
132 spValtrpGlyGlnGlyThrValThrValSerSer 144

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1  ATGAGATTTCGGCTGAGCTGGGTTTCTTGTCTCTTTTGAAGGTGT 50
   |||||
1  MetGluPheGlyLeuSerTrpValPheLeuValAlaIleIleIysGlyVal 17
   |||||
51  CCAGTGTGAGGTCACAGTGTGTGGAGTCTGGGGCGGCTTGGCAAGCCGTG 100
   |||||
17  lGInCysGlnValGlnLeuValGluSerGlyGlyLeuValLysProG 34
   |||||
101  GGGGGTCCCTGAGACTCTGGTGGCGCAGCCTCCGGGTTCAGGTTCACTTC 200
   |||||
34  lYcLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
   |||||
151  AATAACTACTACATGACTGTGGTCCGCCAGGTCTCCAGGCAGGGCGTGCA 200
   |||||
49  SerAspTyrTyrMetSerTrpIleArgGlnAlaProGlyLysGlyLeuG 65
   |||||
201  GTGGGTCTCACGTATTAGTAGTAGTGGTATGCCATGCTACGCAGCAGACT 250
   |||||
65  utrpValSerTyrIleSerSerSerGlySerThrIleTyrTyrAlaAspS 82
   |||||
251  CGGTGAGGGCAGATTCACCATCTCCAGAGAGAAGCCCAACACACACTG 300
   |||||
82  erValIysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
   |||||
301  TTTCTTTCAAATCAACAGCTGAGACTGAGGACACGGCTGCTATTACTG 350
   |||||
99  TyrLeuGlnMetCAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
   |||||
351  TCGCAGCTGTGCATACA..... 366
   |||||
115  sAlaArgValLeuArgPheLeuGluTrpLeuLeuTyrTyrTyrTyrT 132
   |||||
367  ..GGGTCTGACTCTGGGGCCAGGAGTCCTGGTCACCGTCTCCTCA 411
   |||||

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seq\_name: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.US-10-038-591-49

seq\_documentation\_block:  
; Sequence 49, Application US/10038591  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/10/038,591  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 49  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-591-49

alignment\_scores:  
Quality: 532.50 Length: 146  
Ratio: 4.294 Gaps: 3  
Percent Similarity: 84.932 Percent Identity: 73.288  
alignment\_block:  
US-09-019-441-4 x US-10-038-591-49 ..  
Align seg 1/1 to: US-10-038-591-49 from: 1 to: 470

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1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCTGTTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCGTG 100
|||||
17 IclncysGlnAlaGlnLeuValGluSerGlyGlyLeuValLysProG 34
101 GGGGTCCCTGAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||
34 IyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATACTACTACAGTCTGGTCCGCCAGGCTCCAGGCGAGGCGCTGGA 200
|||||
49 SerAspTyrTyrMetSerTrpIleArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGTCTCAGCTATTAGTAGTGGTATCCACATGGTACGCAGACT 250
|||||
65 uTrpValSerTyrIleSerSerSerGlySerThrArgAspTyrAlaAsp 82
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
301 TTCTTCAATGAACAGCTGAGACTGAGGACAGGCTGCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGCAGAGC.....TTGACTACA.....GGTCTG 373
|||||
115 sValArgAspGlyValGluThrPheTyrTyrTyrTyrGlyMeta 132
374 ACTCTGGGGCGAGGAGTCTGGTGGTCCCGTCTCCTCA 411
|||
132 spValTrpGlyGlnGlyThrThrValThrValSerSer 144
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seq\_name: /cgn2\_6/ptodata/2/paa/US097\_COMB.pep.US-09-760-479-636

seq\_name: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.US-10-038-591-45

seq\_documentation\_block:  
; Sequence 45, Application US/10038591  
; GENERAL INFORMATION:  
; APPLICANT: Cohen, Bruce D.  
; APPLICANT: Beebe, Jean  
; APPLICANT: Miller, Penelope E.  
; APPLICANT: Moyer, James D.  
; APPLICANT: Corvalan, Jose R.  
; APPLICANT: Gallo, Michael  
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR  
; FILE REFERENCE: ABX-PF2  
; CURRENT APPLICATION NUMBER: US/10/038,591  
; CURRENT FILING DATE: 2002-01-04  
; PRIOR APPLICATION NUMBER: 60/259,927  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 45  
; LENGTH: 470  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-038-591-45

alignment\_scores:  
Quality: 526.50 Length: 146  
Ratio: 4.246 Gaps: 2  
Percent Similarity: 84.932 Percent Identity: 71.918  
alignment\_block:  
US-09-019-441-4 x US-10-038-591-45 ..  
Align seg 1/1 to: US-10-038-591-45 from: 1 to: 470

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1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTCTGTTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCGTG 100
|||||
17 IclncysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCCCTGAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||
34 IyGlySerLeuArgLeuSerCysThrAlaSerGly.....PheThrPhe 48
151 AATACTACTACAGTCTGGTCCGCCAGGCTCCAGGCGAGGCGCTGGA 200
|||||
49 SerSerTyrAlaMetAsnTrpValArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGTCTCAGCTATTAGTAGTGGTATCCACATGGTACGCAGACT 250
|||||
65 uTrpValSerAlaIleSerGlySerGlyGlyThrThrPheTyrAlaAsp 82
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerArgThrThrLeu 98
301 TTCTTCAATGAACAGCTGAGACTGAGGACAGGCTGCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGCAGAGTTCAGTACAGGCTCTGACTCC..... 378
|||||
115 sAlaLysAspLeuGlyTrpSerAspSerTyrTyrTyrTyrGlyMeta 132
379 .....TGGGGCGAGGAGTCTGGTGGTCCCGTCTCCTCA 411
|||||
132 spValTrpGlyGlnGlyThrThrValThrValSerSer 144
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seq\_documentation\_block:  
; Sequence 636, Application US/09760479  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT253  
; CURRENT APPLICATION NUMBER: US/09/760,479  
; PRIOR FILING DATE: 2001-01-16  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 946  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 636  
; LENGTH: 494  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-479-636

alignment\_scores:  
Quality: 519.00 Length: 145  
Ratio: 4.087 Gaps: 3  
Percent Similarity: 87.586 Percent Identity: 71.724

alignment\_block:  
US-09-019-441-4 x US-09-760-479-636 ..

Align seg 1/1 to: US-09-760-479-636 from: 1 to: 494

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1 ATGGAGTTGGGCTGAGCTGGGTTTCTCTGTTCTTTTGAAGGTGT 50
|||||
22 MetGluPheGlyLeuSerTrpValPheLeuValAlaValLeuLysGlyVa 38
51 CCAGTGTGAGGTGACGTCTGGTGGCTGGGGCGGCTTGGCAAGCCTG 100
|||||
38 IglncysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 55
101 GGGGTCTCCTGAGACTCTGTGTCGAGCTCCGGGTTCCAGGTTACCTTC 150
|||||
55 IyGlySerLeuArgLeuSerCysAlaAlaA.....GluPheAlaPhe 69
151 AATACTACTACAGTACGTGGTCCGCCAGGCTCCAGGGCAGGCTGGA 200
|||||
70 SerAsnTyrTrpMetHisTrpValArgGlnAlaProGlyLysGlyLeu 86
201 GTGGTCTCAGCTATTAGTAGTGTGTGATCCACATGTTGACGAGACT 250
|||||
86 uTrpValSerHisLeuAsnSerAspGlySerSerThrArgTyrAlaAsp 103
251 CCGTGAAGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||
103 erValLysGlyArgPheThrIleSerArgAspAsnValLysAsnThrLeu 119
301 TTTCTTCAATGAACAGCTGAGAGCTGAGACAGCGGTGTCTATTACTG 350
|||||
120 TyrLeuGlnMetSerSerLeuArgValGluAspThrAlaValTyrCy 136
351 TGGC...AGCTGTACTACAGGCTCT.....GACT 376
|||||
136 sAlaArgGlyValLysThrGlySerSerTrpPheSerProAspPheAsp 153
377 CCTGGGCGCAGGAGTCTGTGTACCGTCTCCTCA 411
|||||
153 yrTrpGlyGlnGlyThrLeuValThrValSerSer 164
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seq\_name: /cgn2\_6/ptodata/2/paa/US084\_COMB.pep.us-08-471-986-10

seq\_documentation\_block:  
; Sequence 10, Application US/08471986  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: human monoclonal antibodies and processes and materials for MA  
; NUMBER OF SEQUENCES: 48

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation, Patent Department, K-6-1, 1990  
STREET: 2000 Galloping Hill Road  
CITY: Kenilworth  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07033-0530  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: System Software 7.1  
SOFTWARE: Microsoft Word 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,986  
FILING DATE:  
CLASSIFICATION: 436  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US 94/03429  
FILING DATE: 06-APR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 93400944.0  
FILING DATE: 09-APR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Blasdale, John H. C.  
REGISTRATION NUMBER: 31,895  
REFERENCE/DOCKET NUMBER: SF0368KG1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 908-298-2902  
TELEFAX: 908-298-5388  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 138 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-471-986-10

alignment\_scores:  
Quality: 518.50 Length: 140  
Ratio: 4.115 Gaps: 2  
Percent Similarity: 90.000 Percent Identity: 72.143

alignment\_block:  
US-09-019-441-4 x US-08-471-986-10 ..

Align seg 1/1 to: US-08-471-986-10 from: 1 to: 138

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1 ATGGAGTTGGGCTGAGCTGGGTTTCTCTGTTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpPheLeuValAlaPheLeuLysGlyVa 17
51 CCAGTGTGAGGTGACGTCTGGTGGCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 IglncysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCTCCTGAGACTCTGTGTCGACGCTCCGGGTTCCAGGTTACCTTC 150
|||||
34 IyGlySerLeuArgLeuSerCysValGlySerGly.....PheThrPhe 48
151 AATACTACTACAGTACGTGGTCCGCCAGGCTCCAGGGCAGGCTGGA 200
|||||
49 ThrAsnTyrAlaMetThrTrpValArgGlnAlaProGlyLysGlyLeu 65
201 GTGGTCTCAGCTATTAGTAGTGTGTGATCCACATGTTGACGAGACT 250
|||||
65 uTrpValSerAlaIleSerGlySerGlyAsnTyrThrTyrSerAsp 82
251 CCGTGAAGCGCAGATTCCACATCTCCAGAGAGAACGCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysSerThrLeu 98
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```

301 TTCTTCATGAACAGCCCTGAGAGCTGAGACACGGCTCTCTATTACTG 350
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
99  TyrLeuHisMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrCy 115
   ::::::::::::::::::::::::::::::::::::::::::::::::::
351 TGGCAGCTTGACTACAGGGTCT.....GACTCTCTGGGGCCAGGGAG 391
   :::::::::::::::::::: :::: :::: :::: :::: :::: ::::
115 sAlaLysAlaAlaValHisAlaTyrPheAspTyrTrpGlyGlnGlyT 132
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
392 TCCTGGTCACCGTCTCTCTCA 411
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
132 hrLeuValThrValSerSer 138
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seq_name: /cgn2_6/ptodata/2/paa/US60_COMB.pep:US-60-214-601-15

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seq_documentation_block:
; Sequence 15, Application US/60214601
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Lu, Dyung Aina M.
; APPLICANT: Lal, Preeti
; APPLICANT: Batra, Sajeev
; APPLICANT: Burford, Neil
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Nguyen, Daniel B.
; APPLICANT: Azimzai, Yalda
; APPLICANT: Yao, Monique G.
; APPLICANT: Wallia, Narinder K.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PF-0789 P
; CURRENT APPLICATION NUMBER: US/60/214,601
; CURRENT FILING DATE: 2000-06-27
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 15
; LENGTH: 519
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 3506590CD1
US-60-214-601-15

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alignment_scores:
  Quality: 517.50      Length: 144
  Ratio: 4.277        Gaps: 2
  Percent Similarity: 84.028      Percent Identity: 71.528

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alignment_block:
US-09-019-441-4 x US-60-214-601-15 ..

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Align seg 1/1 to: US-60-214-601-15 from: 1 to: 519
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1  ATGAGATTGGGCTGAGCTGGGTTTCTCTGCTCTCTTTTGAAGCTGT 50
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
1  MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa 17
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
51  CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTG 100
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
17  lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
101  GGGGGTCCCTGAGACTCTGTGTGCAGCCCTCCGGGTTTCAGGTTTCACCTTC 150
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
34  lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
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151  AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
   :::::::::: :::: :::: :::: :::: :::: ::::
49  SerSerTyrAlaMetHisTrpValArgGlnAlaProGlyLysGlyLeuGl 65
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
201  GTGGGTCTCAGCTATTAGTAGTGTGTGATCCACATGGTGTACGAGACT 250
   ||||| :::::::::: :::: :::: :::: :::: ::::
65  utrPValAlaValIleSerTyrAspGlySerAsnLysTyrTyrAlaAspS 82
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::

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251  CCGTGAAGGCCAGATTCAACCATCTCCAGAGAGAACGCCACACACACTG 300
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
82  erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
   ::::::::::::::::::::::::::::::::::::::::::::::::::
301  TTCTTCATGAACAGCCCTGAGAGCTGAGACACGGCTCTCTATTACTG 350
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99  TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
351  TGGCAGCTTGACTACAGGGTCT.....GACTCTCT 379
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
115  sAlaArgAlaGlyGluGlySerProAspThrLeuValAlaPheAspIleT 132
   ::::::::::::::::::::::::::::::::::::::::::::::::::::
380  GGGGCCAGGAGTCCCTGGTCACCGTCTCTCTCA 411
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132  rpGlyGlnGlyThrMetValThrValSerSer 142
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; Sequence 77, Application US/09269332
; GENERAL INFORMATION:
; APPLICANT: SATO, KOH
; APPLICANT: WAKAHARA, YUJI
; APPLICANT: YABUTA, NAOTIRO
; TITLE OF INVENTION: ANTIBODY AGAINST HUMAN PARATHORMONE RELATED PEPTIDES
; FILE REFERENCE: 04853-0033
; CURRENT APPLICATION NUMBER: US/09/269,332
; CURRENT FILING DATE: 1999-03-25
; PRIOR APPLICATION NUMBER: PCT/JP97/03382
; PRIOR FILING DATE: 1997-09-24
; PRIOR APPLICATION NUMBER: JP 255196/1996
; PRIOR FILING DATE: 1996-09-26
; PRIOR APPLICATION NUMBER: JP 214168/1997
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-269-332-77

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alignment_scores:
  Quality: 515.00      Length: 139
  Ratio: 4.221        Gaps: 2
  Percent Similarity: 87.770      Percent Identity: 74.101

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alignment_block:
US-09-019-441-4 x US-09-269-332-77 ..

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1  ATGAGATTGGGCTGAGCTGGGTTTCTCTGCTCTCTTTTGAAGCTGT 50
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1  MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa 17
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51  CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGCGGCTTGGCAAAGCCTG 100
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17  lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
101  GGGGGTCCCTGAGACTCTGTGTGCAGCCCTCCGGGTTTCAGGTTTCACCTTC 150
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
34  lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
151  AATAACTACTACATGGACTGGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
   :::::::::: :::: :::: :::: :::: :::: ::::
49  SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
   ||||| ::::::::::::::::::::::::::::::::::::::::::::::
201  GTGGGTCTCAGCTATTAGTAGTGTGTGATCCACATGGTGTACGAGACT 250
   ||||| :::::::::: :::: :::: :::: :::: ::::
65  utrPValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAspS 82
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251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300  
|||||  
82 erVallysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
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301 TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGCTCTCTATTACTG 350  
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99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrcy 115  
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115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132  
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395 TGCTCACCTCTCTCTCA 411  
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132 euValThrValSerSer 137

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seq\_documentation\_block:  
; Sequence 77, Application US/09423800  
; GENERAL INFORMATION:  
; APPLICANT: SATO, KOH  
; APPLICANT: TSUNENARI, TOSHIAKI  
; APPLICANT: ISHII, KIMIE  
; TITLE OF INVENTION: CACHEXIA REMEDY  
; FILE REFERENCE: 04853-0036  
; CURRENT APPLICATION NUMBER: US/09/423.800  
; CURRENT FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: PCT/JP98/02116  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: JP 125505/1997  
; PRIOR FILING DATE: 1997-05-15  
; PRIOR APPLICATION NUMBER: JP 194445/1997  
; PRIOR FILING DATE: 1997-07-18  
; NUMBER OF SEQ ID NOS: 87  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 77  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-423-800-77

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Quality: 515.00 Length: 139  
Ratio: 4.221 Gaps: 2  
Percent Similarity: 87.770 Percent Identity: 74.101

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1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50  
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1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa 17  
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51 CCAGTGTGAGGTGAGCTGTGTGAGTGTGGGGCGGCTTGGCAAAGCTG 100  
|||||  
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG 34  
|||||  
101 GGGGGTCCCTGAGACTGTGTGGCGGACCTCCGGGTTTCAGGTTTCACCTTC 150  
|||  
34 lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
|||||  
151 AATAACTACTACATGAGCTGGGTCGCCAGGCTCCAGGGCAGGGGTGGA 200  
|||||  
49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65  
|||||  
201 GTGGGTCTCAGCTATTAGTAGTGGTATCCACATGTCACGACGACT 250  
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65 utrPValAlaThrIleSerSerGlyGlySerTyrThrTyrProAspS 82

251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACTG 300  
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82 erVallysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
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301 TTTCTTCAAAATGAACAGCCTGAGAGCTGAGGACACGCTCTCTATTACTG 350  
|||||  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrcy 115  
|||||  
351 TGGCAGCTTGACATACAGGGTCT.....GACTCCTGGGGCCAGGGAGTCC 394  
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115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132  
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395 TGCTCACCTCTCTCTCA 411  
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seq\_name: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pap:PCT-US01-18569-4273  
seq\_documentation\_block:  
; Sequence 4273, Application PC/TUS0118569  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA133PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/18569  
; CURRENT FILING DATE: 2001-06-07  
; PRIOR APPLICATION NUMBER: 60/209,467  
; PRIOR FILING DATE: 2000-06-07  
; NUMBER OF SEQ ID NOS: 4360  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 4273  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: SITE  
; LOCATION: (184)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (187)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US01-18569-4273

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Quality: 507.50 Length: 138  
Ratio: 4.126 Gaps: 2  
Percent Similarity: 89.130 Percent Identity: 70.290

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22 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLysGlyVa 38  
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51 CCAGTGTGAGGTGAGCTGTGTGAGTGTGGGGCGGCTTGGCAAAGCTG 100  
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38 lGlnCysGlnValGlnLeuValGluSerGlyGlyGlyLeuValLysProG 55  
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101 GGGGGTCCCTGAGACTGTGTGGCGGACCTCCGGGTTTCAGGTTTCACCTTC 150  
|||||  
55 lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 69  
|||||  
151 AATAACTACTACATGAGCTGGGTCGCCAGGCTCCAGGGCAGGGGTGGA 200  
|||||  
70 SerAspPheTyrMetSerTrpIleArgGlnValProGlyLysGlyLeuG 86  
|||||  
201 GTGGGTCTCAGCTATTAGTAGTGGTATCCACATGTCACGACGACT 250  
|||||





201 GTGGGTCTCACGTATTAGTAGTGGTGATCCACATGGTAGCAGACT 250  
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65 utrValAlaAsnIleAsnProAspGlySerGlnSerArgTyrValAsps 82  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
251 CGGTGAAGGGCAGATTCCACATCTCCAGAGAGAGCCCAACACACACTG 300  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
82 erValLysGlyArgPheThrValSerArgAspAsnAlaLysLysSerLeu 98  
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99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaIleTyrTyCy 115  
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351 TCCGAGCTTGACTACAGGCTCTGACTCTGGGGCCAGGAGTCCTGGTCA 400  
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115 sleuGlyTrpSerAlaProAlaAlaProtrpGlyGlnGly.ThrTrpSer 131  
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132 ProSerPro 134

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seq\_documentation\_block:  
; Sequence 13609, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US1.PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13609  
; LENGTH: 137  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -19..-1  
US-60-197-873-13609

alignment\_scores:  
Quality: 504.00 Length: 137  
Ratio: 4.065 Gaps: 2  
Percent Similarity: 90.511 Percent Identity: 68.613

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51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCAAGGCTG 100  
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17 lGlnCysGluValGlnValGluSerGlyGlyGlyLeuValGlnProG 34  
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34 lYglySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
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65 utrValAlaAsnIleAsnProAspGlySerGlnSerArgTyrValAsps 82  
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; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL MACROPHAGE NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-065  
; CURRENT APPLICATION NUMBER: PCT/US01/08655  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 09/522,929  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/770,160  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/668,317  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,783  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: 09/728,628  
; PRIOR FILING DATE: 2000-12-01  
; PRIOR APPLICATION NUMBER: 09/783,066  
; PRIOR FILING DATE: 2001-02-13  
; PRIOR APPLICATION NUMBER: 09/816,828  
; PRIOR FILING DATE: 2001-03-22  
; NUMBER OF SEQ ID NOS: 584  
; SOFTWARE: Custom  
; SEQ ID NO 218  
; LENGTH: 136  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US01-08655-218

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Percent Similarity: 93.220 Percent Identity: 82.203

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51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGCGGCTTGCAAGGCTG 100  
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17 lGlnCysGluValGlnLeuValGluSerGlyGlyGlyLeuValGlnProG 34  
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Date: Sep 23, 2002 9:59 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Search information block:

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Database sequences: 949130  
Database length: 267991220  
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/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-91409 +		534.00	832.83	5,2e-38	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88099 +		534.00	832.44	5,2e-38	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88538 +		533.50	832.11	5,7e-38	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-102578 +		533.00	831.80	6,3e-38	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-19882 +		529.50	826.05	1,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-102501 +		529.50	825.99	1,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-102647 +		529.50	825.28	1,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-19817 +		528.50	824.49	1,5e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88399 +		528.50	824.43	1,5e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88960 +		528.50	824.21	1,5e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-45754 +		528.50	823.88	1,6e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-102430 +		527.00	822.04	2,1e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-19891 +		526.50	821.73	2,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-30713 +		526.50	821.32	2,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-117589 +		526.50	820.60	2,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88895 +		524.50	818.09	3,4e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-105249 +		524.50	817.49	3,4e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-16950 +		524.00	817.37	3,8e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-102479 +		522.00	814.37	5,7e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-30682 +		522.00	814.25	5,7e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-104928 +		521.50	813.03	6,3e-37	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-88985 +		519.00	809.58	1,0e-36	
/cgn2_6/ptodata1/paa/US10_NEW_COMB.ppt:US-10-206-008-636 +		519.00	799.46	1,1e-36	
/cgn2_6/ptodata1/paa/US09_NEW_COMB.ppt:US-09-791-537-19919 +		518.00	808.14	1,3e-36	

/cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-19837 + 517.00 806.81 1,5e-3  
/cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-88849 + 517.00 806.46 1,5e-3  
/cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-29476 + 517.00 805.97 1,5e-3  
/cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-30736 + 516.50 805.63 1,7e-3  
/cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-60943 + 516.50 805.08 1,7e-3

seq\_name: /cgn2\_6/ptodata1/paa/US09\_NEW\_COMB.ppt:US-09-791-537-88908

seq\_documentation\_block:

; Sequence 88908, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 88908  
; LENGTH: 143  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-791-537-88908

alignment\_scores:

Quality: 547.50 Length: 144  
Ratio: 4.345 Gaps: 2  
Percent Similarity: 87.500 Percent Identity: 74.306

alignment\_block:

US-09-019-441-4 x US-09-791-537-88908 ..  
Align seg 1/1 to: US-09-791-537-88908 from: 1 to: 143  
1 ATGAGATTGGCGTGGAGCTGGTGGTTTCCTCTCTTTTGAAGGTGT 50  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17  
51 CCAGTGTGAGCTGAGCTGGTGGAGTCTGGGGGGCTGGCAAGCCTG 100  
17 lglCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34  
101 GGGGTCCTCCAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTC 150  
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATACTACTACATGGAGCTGGTGGTCCGCCAGGCTCCAGGAGGGCTGGA 200  
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGGTCTCAGCTATTAGTACTAGTGGTGATCCACATGGTACGAGACT 250  
65 utrPValSerAlaIleThrGlySerGlySerThrTyrTyrAlaAsps 82  
251 CCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTCTTCAATGACAGCTCGAGAGCTGAGGACAGGCTGCTATTACTG 350  
TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115  
351 TGCAGC.....TTGACTACAGGGTCTGACTCCT 379  
115 sAlaLysAlaSerIleArgThrValValThrProGlyPheAspTyrT 132  
380 GGGCCAGGGAGTCTGGTGGTACCGGCTCCTCA 411  
132 rpGlyGlnGlyThrLeuValThrValSerSer 142

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pap:US-09-791-537-19856

seq\_documentation\_block:

; Sequence 19856, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 19856

; LENGTH: 138

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-19856

alignment\_scores:

Quality: 546.50 Length: 140

Ratio: 4.372 Gaps: 2

Percent Similarity: 89.286 Percent Identity: 76.429

alignment\_block:

US-09-019-441-4 x US-09-791-537-19856

Align seg 1/1 to: US-09-791-537-19856 from: 1 to: 138

1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTCTCTTTTAAAGGTGT 50

1 MetGluPheGlyLeuSerTrpLeuValAlaIleLeuLysGlyVa 17

51 CCAGTGTGAGGTGAGCTGGTGGATCTGGGGCGGCTTGGCAAGCCTG 100

17 IclnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34

101 GGGGTCTCCTGAGACTCTGTGTCGCGAGCTCCGGGTTCCAGTTACCTTC 150

34 IyGlySerLeuArgLeuSerCysAlaIleSerGly.....PheThrPhe 48

151 AATACTACTACATGAGCTGGTCCGCGAGCTCCAGGCGAGGCTCGA 200

49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65

201 GTGGTCTCAGCTATTAGTAGTGTGTATCCACATGGTACGAGACT 250

65 utrPvalSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsps 82

251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCCCAACACACTG 300

82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98

301 TTTCTTCAATGAACAGCTGAGCTGAGGCTGAGGCTGCTATTACTG 350

99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115

351 TCGGAGCTTGACTACAGG.....TCTGACTCTCCGGGCGGAGGAG 391

115 salAlaLysAlaArgThrGlyTyrTrpTyrPheAspLeuTrpGlyArgGly 132

392 TCCTGGTCCAGCTCTCTCA 411

132 hrLeuValThrValSerSer 138

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pap:US-09-791-537-19722

seq\_documentation\_block:

; Sequence 19722, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 19722

; LENGTH: 145

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-19722

alignment\_scores:

Quality: 544.50 Length: 140

Ratio: 4.356 Gaps: 2

Percent Similarity: 89.286 Percent Identity: 76.429

alignment\_block:

US-09-019-441-4 x US-09-791-537-19722

Align seg 1/1 to: US-09-791-537-19722 from: 1 to: 145

1 ATGGAGTTTGGGCTGAGCTGGGTTTTCCTTGTCTCTTTTAAAGGTGT 50

8 MetGluPheGlyLeuSerTrpLeuValAlaIleLeuLysGlyVa 24

51 CCAGTGTGAGGTGAGCTGGTGGAGCTGGGGCGGCTTGGCAAGCCTG 100

24 IclnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 41

101 GGGGTCTCCTGAGACTCTGTGTCGCGAGCTCCGGGTTCCAGTTACCTTC 150

41 IyGlySerLeuArgLeuSerCysAlaIleSerGly.....PheThrPhe 55

151 AATACTACTACATGAGCTGGTCCGCGAGCTCCAGGCGAGGCTCGA 200

56 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 72

201 GTGGTCTCAGCTATTAGTAGTGTGTATCCACATGGTACGAGACT 250

72 utrPvalSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsps 89

251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAGCCCAACACACTG 300

89 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 105

301 TTTCTTCAATGAACAGCTGAGCTGAGGCTGAGGCTGCTATTACTG 350

106 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 122

351 T.....CCGAGCTTGACTACAGGCTGCTGACTCTCTGGGCGGAGGAG 391

122 salAlaLysAspAlaGlyTrpGlySerGlyPheAspTyrTrpGlyGlnGly 139

392 TCCTGGTCCAGCTCTCTCA 411

139 hrLeuValThrValSerSer 145

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pap:US-09-791-537-102425

seq\_documentation\_block:

; Sequence 102425, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

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; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102425
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-102425
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alignment_scores:
  Quality: 542.50      Length: 140
  Ratio: 4.375        Gaps: 2
  Percent Similarity: 88.571  Percent Identity: 75.000

alignment_block:
US-09-019-441-4 x US-09-791-537-102425 ..
Align seg 1/1 to: US-09-791-537-102425 from: 1 to: 139
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1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTGTCTCTTTTGAAGGTGT 50
|||||
1 MetCluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGlyVa 17
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTG 100
|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyLeuValLysProG 34
101 GGGGGTCCCTGAGACTCTGTGGCCAGCTCCGGGTTACAGTTCACCTTC 150
|||||
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGCTGGTGGCCAGCTCCAGGCGAGGGCTGGA 200
|||||
49 SerAspTyrTyrMetThrTrpIleArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGGTCTCACGTATTAGTAGTGTGTGATCCACATGTCACGAGACT 250
|||||
65 uTrpLeuSerTyrLeuSerSerSerGlyArgThrIleTyrTyrAlaAsp 82
251 CCGTGAAGGCAGATTACCATCTCCAGAGAGACGCCACACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
301 TTTCTTCAAAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTG 350
|||||
99 PheLeuGlnThrAsnAsnLeuArgAlaGluAspThrAlaValTyrTyrCy 115
351 TGCAGAGCTTCACTACAGGCT.....GACTCTGGGGCCAGGAG 391
|||||
115 sAlaArgValTyrSerSerSerTrpGluPheAspTyrTrpGlyGlnGlyT 132
392 TCCTGGTCCAGCTCTCTCA 411
132 hrLeuValThrValSerSer 138
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88984
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seq_documentation_block:
; Sequence 88984, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBR
; FILE REFERENCE: 261/210
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88984
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-88984
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alignment_scores:
  Quality: 542.50      Length: 142
  Ratio: 4.272        Gaps: 3
  Percent Similarity: 89.437  Percent Identity: 76.761
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alignment_block:
US-09-019-441-4 x US-09-791-537-88984 ..
Align seg 1/1 to: US-09-791-537-88984 from: 1 to: 141

1 ATGGAGTTTGGGCTGAGCTGGGTTTTCTTGTCTCTTTTGAAGGTGT 50
|||||
1 MetCluPheGlyLeuSerTrpLeuPheValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCTG 100
|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
101 GGGGGTCCCTGAGACTCTGTGGCCAGCTCCGGGTTACAGTTCACCTTC 150
|||||
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGCTGGTGGCCAGCTCCAGGCGAGGGCTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGGTCTCACGTATTAGTAGTGTGTGATCCACATGTCACGAGACT 250
|||||
65 uTrpValSerAlaIleSerGlySerGlyGlySerTyrTyrTyrAlaAsp 82
251 CCGTGAAGGCAGATTACCATCTCCAGAGAGACGCCACACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAAAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
351 TGCAGAGCTT...ACTACAGGCTCTGACTCC.....TGGGGCC 385
|||||
115 sAlaLysLeuSerThrThrValThrArgSerTyrGlyValTyrTrpGlyG 132
386 AGGAGTCTCTGGTCACCGTCTCTCA 411
132 lNGLyThrLeuValThrValSerSer 140
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-102457
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seq_documentation_block:
; Sequence 102457, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 102457
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-791-537-102457

alignment\_scores:  
Quality: 541.50 Length: 140  
Ratio: 4.332 Gaps: 2  
Percent Similarity: 89.286 Percent Identity: 75.714  
alignment\_block:  
US-09-019-441-4 x US-09-791-537-102457 ..  
Align seg 1/1 to: US-09-791-537-102457 from: 1 to: 139

1 ATGGAGTTTGGGTGAGCTGGGTTTCCTTCCTCTTTTGAAGGTGT 50  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuGlyGlyVa 17  
51 CCAGTGTGAGGTGAGCTGGTGGGCTGGGGCGGCTGGCAAGCCTG 100  
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTGCTGGTGGCCAGCCTCCGGGTTACAGTTACCTTC 150  
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGAGCTGGTGGCCAGCCTCCGGGTTACAGTTACCTTC 150  
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGGTCTCACGTATTAGTAGTGGTCCAGGCTCCAGGCGAGGGCTGGA 200  
65 utrPValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsp 82  
251 CGGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACACACACTG 300  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115  
351 TCGGAGCTTGACTACAGGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350  
115 salAlaLys.....AspGlyGlyValTyrTrpGlyGlnGlyThrLeuValT 130  
392 TCCTGTCACCGTCTCCCTCA 411  
132 hrThrValThrValSerSer 138

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-89386

seq\_documentation\_block:  
; Sequence 89386, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBERS  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 89386  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-89386

alignment\_scores:  
Quality: 540.00 Length: 137

Ratio: 4.355 Gaps: 2  
Percent Similarity: 90.511 Percent Identity: 77.372

alignment\_block:  
US-09-019-441-4 x US-09-791-537-89386 ..

Align seg 1/1 to: US-09-791-537-89386 from: 1 to: 134

1 ATGGAGTTTGGGTGAGCTGGGTTTCCTTCCTCTTTTGAAGGTGT 50  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuGlyGlyVa 17  
51 CCAGTGTGAGGTGAGCTGGTGGGCTGGGGCGGCTGGCAAGCCTG 100  
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTGCTGGTGGCCAGCCTCCGGGTTACAGTTACCTTC 150  
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGAGCTGGTGGCCAGCCTCCAGGCGAGGGCTGGA 200  
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGGTCTCACGTATTAGTAGTGGTCCAGGCTCCAGGCGAGGGCTGGA 200  
65 utrPValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsp 82  
251 CGGTGAAGGGCAGATTCACCATCTCCAGAGAACGCCAACACACACTG 300  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTCTTCAATGAACAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115  
351 TCGGAGCTTGACTACAGGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350  
115 salAlaLys.....AspGlyGlyValTyrTrpGlyGlnGlyThrLeuValT 130  
401 CGGCTCTCTCA 411  
130 hrValSerSer 133

seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-72392

seq\_documentation\_block:  
; Sequence 72392, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 72392  
; LENGTH: 156  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-72392

alignment\_scores:  
Quality: 539.50 Length: 140  
Ratio: 4.316 Gaps: 2  
Percent Similarity: 89.286 Percent Identity: 75.714  
alignment\_block:  
US-09-019-441-4 x US-09-791-537-72392 ..

Align seg 1/1 to: US-09-791-537-72392 from: 1 to: 156

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1 ATGGAGTTGGCTGAGCTGGGTTTCCTTCTGTCCTTTTCAAGGTC 50
|||||
19 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaLeuLysGlyVa 35
|||||
51 CCAGTGTGAGTGCAGCTGGTGGAGCTCTGGGGCGGCTTGCAAGCCTG 100
|||||
35 lClnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 52
|||||
101 GGGGTCCTCAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||
52 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 66
|||||
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||
67 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 83
|||||
201 GTGGTCTCAGCTATTAGTAGTGGTGATCCACATGTCACGAGACT 250
|||||
83 utrPValSerAlaLeSerGlySerGlySerThrTyrTyrAlaAsps 100
|||||
251 CGGTCAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||
100 erValLysGlyArgPheThrLeSerArgAspAsnSerLysAsnThrLeu 116
|||||
301 TTCTTCAATCAACAGCTCAGAGCTGAGGACGAGCTGCTCTATTACTG 350
|||||
117 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 133
|||||
351 TCCGAGCTTGACTACAGGCTCT.....GACTCTGGGGCCAGGAG 391
|||||
133 salAlLysAspTrpAsnAspAsnTrpPheAspProTrpGlyGlnGlyT 150
|||||
392 TCCTGCTCAGCTCTCCCTCA 411
|||||
150 hrLeuValThrValSerSer 156
|||||
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-36911

seq\_documentation\_block:

; Sequence 36911, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 36911

; LENGTH: 160

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-36911

alignment\_scores:  
Quality: 538.50 Length: 146  
Ratio: 4.308 Gaps: 2  
Percent Similarity: 85.616 Percent Identity: 72.603

alignment\_block:

US-09-019-441-4 x US-09-791-537-36911 ..

Align seg 1/1 to: US-09-791-537-36911 from: 1 to: 160

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1 ATGGAGTTGGCTGAGCTGGGTTTTCCTTCTGTCCTTTTCAAGGTC 50
|||||
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```
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaLeuLysGlyVa 17
51 CCAGTGTGAGCTGAGCTGGTGGAGCTCTGGGGCGGCTTGCAAGCCTG 100
|||||
17 lClnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
|||||
101 GGGGTCCTCAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
|||||
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||
49 SerThrTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
|||||
201 GTGGTCTCAGCTATTAGTAGTGGTGATCCACATGTCACGAGACT 250
|||||
65 utrPValSerAlaLeSerGlySerGlySerThrTyrTyrAlaAsps 82
|||||
251 CCGTCAAGGCGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||
82 erValLysGlyArgPheThrLeSerArgAspAsnSerLysAsnThrLeu 98
|||||
301 TTCTTCAATCAACAGCTCAGAGCTGAGGACGAGCTGCTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
|||||
351 TCCGAGCTTGACTACA.....GGGTCGTG 373
|||||
115 salAlLysAlaValValArgGlyValLeSerTyrTyrTyrGlyMetAl 132
|||||
374 ACTCCTGGGGCCAGGAGCTCTGCTCAGCTCCTCTCA 411
|||||
132 spValTrpGlyGlnGlyThrThrValThrValSerSer 144
|||||
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-51417

seq\_documentation\_block:

; Sequence 51417, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 51417

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-51417

alignment\_scores:  
Quality: 538.50 Length: 146  
Ratio: 4.308 Gaps: 2  
Percent Similarity: 85.616 Percent Identity: 72.603

alignment\_block:  
US-09-019-441-4 x US-09-791-537-51417 ..

Align seg 1/1 to: US-09-791-537-51417 from: 1 to: 161

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1 ATGGAGTTGGCTGAGCTGGGTTTTCCTTCTGTCCTTTTCAAGGTC 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaLeuLysGlyVa 17
|||||
51 CCAGTGTGAGTGCAGCTGGTGGAGCTCTGGGGCGGCTTGCAAGCCTG 100
|||||
17 lClnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
|||||
```

```
101 GGGGGTCCCTGAGACTGTGGTCCGAGCTCCGGGTTACAGTTCACCTTC 150
|||||
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PhethrPhe 48
|||||
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGGTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
|||||
201 GTGGGTCTCAGCTATTAGTAGTGGTATCCACATGGTACGCAGACT 250
|||||
65 utrPValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAspS 82
|||||
251 CGGTGAAGGCAGATTCACCATCTCCAGAGACAGCCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||
351 TCGGAGCTTGACTACA.....TTGACTACAGGCTCTGACTCCTCGG 373
|||||
115 salalysAlaValAlaValArgGlyValIleSerTyrTyrTyrGlyMeta 132
|||||
374 ACTCGTGGGGCCAGGAGCTCGTGGTCACGCTCCTCTCA 411
|||
132 spValTrpGlyGlnGlyThrValThrValSer 144
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seq_name: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:PCT-US02-20181-2
seq_documentation_block:
; Sequence 2, Application PC/TUS0220181
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPGL
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: PCT/US02/20181
; CURRENT FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2002-06-25
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
PCT-US02-20181-2
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alignment_scores:
  Quality: 537.00      Length: 143
  Ratio: 4.296        Gaps: 2
Percent Similarity: 87.413 Percent Identity: 73.427
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alignment_block:
US-09-019-441-4 x PCT-US02-20181-2
Align seg 1/1 to: PCT-US02-20181-2 from: 1 to: 467
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1 ATGAGATTGGGCTGAGCTGGGTTTCTCTTCTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17
|||||
51 CCAGTGTGAGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnPro 34
|||||
101 GGGGGTCCCTGAGACTCTGGTGGCAGCTCCGGGTTACAGTTCACCTTC 150
|||||
```

```
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PhethrPhe 48
|||||
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGGTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
|||||
201 GTGGGTCTCAGCTATTAGTAGTGGTATCCACATGGTACGCAGACT 250
|||||
65 utrPValSerGlyIleThrGlySerGlySerThrTyrTyrAlaAspS 82
|||||
251 CGGTGAAGGCAGATTCACCATCTCCAGAGACAGCCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||
351 TCGGAGC.....TTGACTACAGGCTCTGACTCCTCGG 382
|||||
115 salalysAspProGlyThrThrValIleMetSerTrpPheAspProTrpG 132
|||||
383 GCAGGGAGTCTGCTGCTACCGTCTCCTCA 411
|||||
132 lyGlnGlyThrLeuValThrValSer 141
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seq_name: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:US-09-791-537-88448
seq_documentation_block:
; Sequence 88448, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 88448
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-88448
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alignment_scores:
  Quality: 536.00      Length: 145
  Ratio: 4.323        Gaps: 2
Percent Similarity: 85.517 Percent Identity: 73.103
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alignment_block:
US-09-019-441-4 x US-09-791-537-88448
Align seg 1/1 to: US-09-791-537-88448 from: 1 to: 144
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1 ATGAGATTGGGCTGAGCTGGGTTTCTCTTCTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17
|||||
51 CCAGTGTGAGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnPro 34
|||||
101 GGGGGTCCCTGAGACTCTGGTGGCAGCTCCGGGTTACAGTTCACCTTC 150
|||||
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PhethrPhe 48
|||||
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGCGAGGGGTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
```



```
201 GTGGTCTCAGCTATTAGTAGTGGTGATGCCACATGGTACGAGACT 250
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
65 uTrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAsps 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
251 CCGTGAAGGCGGAGTTCACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
82 erValLysArgArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
301 TTCTTCAATGAACAGCTGAGAGCTGAGGACACGCGTGTCTATTACTG 350
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
351 TCCGAGCTTGACTACAGG.....TCTGACT 376
|||||  |||
115 sAlaLysAlaGlnArgGlyGlyHisThrAlaMetValProTrpGlyAspt 132
|||||  |||
377 COTGGGCGCAGGAGTCTCTGTCACCGTCTCTCTCA 411
|||||  |||
132 yrTrpGlyGlnGlyThrLeuValThrValSerSer 143
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-39928

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seq_documentation_block:
; Sequence 39928, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 39928
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-39928
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alignment_scores:
  Quality: 536.00      Length: 143
  Ratio: 4.288        Gaps: 2
Percent Similarity: 87.413 Percent Identity: 74.825
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alignment\_block:

US-09-019-441-4 x US-09-791-537-39928

Align seg 1/1 to: US-09-791-537-39928 from: 1 to: 148

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1 ATGGAGTTTGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 MetGluLeuGlyLeuArgTrpValPheLeuValAlaIleLeuGluGlyVa 17
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 CCAGTGTGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 34
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 GGGGTCCTTGAGACTCTGGTCCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 lyGlySerLeuArgLeuSerCysAlaLaSerGly.....PheThrPhe 48
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
151 AATAACTACTACAGTCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
49 SerSerTyrSerMetAsnTrpValargGlnAlaProGlyLysGlyLeuGl 65
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
201 GTGGTCTCAGCTATTAGTAGTGGTGATGCCACATGGTACGAGACT 250
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
65 uTrpValSerIleSerSerSerSerSerTyrIleTyrTyrAlaAsps 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
```

```
251 CCGTGAAGGCGGAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
301 TTCTTCAATGAACAGCTGAGAGCTGAGGACACGCGTGTCTATTACTG 350
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
351 TCCGAGC.....TTGACTACAGGCTCTGACTCTCTGGG 382
|||||  |||
115 sAlaArgAspLeuArgGlyGlnTrpLeuValGlnGlyGluAspTyrTrpG 132
|||||  |||
383 GCCAGGAGTCTCTGTCACCGTCTCTCTCA 411
|||||  |||
132 lyGlnGlyThrLeuValThrValSerSer 141
|||||  |||
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-16931

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seq_documentation_block:
; Sequence 16931, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16931
; LENGTH: 141
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-16931
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alignment_scores:
  Quality: 535.50      Length: 142
  Ratio: 4.319        Gaps: 2
Percent Similarity: 87.324 Percent Identity: 74.648
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alignment\_block:

US-09-019-441-4 x US-09-791-537-16931

Align seg 1/1 to: US-09-791-537-16931 from: 1 to: 141

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1 ATGGAGTTTGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
51 CCAGTGTGAGGTGACGTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
101 GGGGTCCTTGAGACTCTGGTCCGAGCTCCGGGTTTCAGGTTACCTTC 150
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
34 lyGlySerLeuArgLeuSerCysAlaLaSerGly.....PheThrPhe 48
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
151 AATAACTACTACAGTCTGGTCCGCCAGGCTCCAGGCGAGGGCTGGA 200
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
49 SerSerTyrAlaMetSerTrpValargGlnAlaProGlyLysGlyLeuGl 65
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
201 GTGGTCTCAGCTATTAGTAGTGGTGATGCCACATGGTACGAGACT 250
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
65 uTrpValSerAlaIleSerGlySerGlyGlySerThrTyrTyrAlaAsps 82
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
251 CCGTGAAGGCGGAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTG 300
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
301 TTCTTCAATGAACAGCTTGAGACTGAGGACACGCGTGTCTATTACTG 350
|||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||  |||||||
```

```

99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGGCAGCTTG.....ACTACAGGCTCTGACTCTGGGCC 385
115 sAlaLysAlaHisTyrAspPheTrpSerGlyTyrTyrAspTyrTrpGly 132
386 AGGAGTCCTGGTCACCGTCTCCTCA 411
132 lnGlyThrLeuValThrValSer 140
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seq\_name: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep:US-09-791-537-106513

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seq_documentation_block:
; Sequence 106513, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 106513
; LENGTH: 150
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-106513
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alignment\_scores:
Quality: 535.50 Length: 152
Ratio: 4.250 Gaps: 3
Percent Similarity: 82.895 Percent Identity: 71.711

alignment\_block:
US-09-019-441-4 x US-09-791-537-106513 ..
Align seg 1/1 to: US-09-791-537-106513 from: 1 to: 150
1 ATGGAGTTTGGGCTGAGTGGGTTTCCTCTCTCTTTGAAAGTGT 50
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCCTG 100
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCCTCCTGAGACTCTGGTCGCGAGCTCCGGGTTTCAGGTTACCTTC 150
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATACTACTACATGAGTCTGGTCCGCGAGCTCCAGGCTCCAGGGCGGCTGA 200
49 SerSerTyrTrpMetHisTrpValArgGlnAlaProGlyLysGlyLeuVa 65
201 GTGGGCTCAGCTATTAGTAGTAGTGGTATCCACATGGTACGAGACT 250
65 lTrpValSerArgIleAsnSerAspGlySerSerThrSerTyrAlaAsps 82
251 CCGTGAAGGGCAGATTCCACCATCTCCAGAGAGAACGCCAACACACTG 300
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 98
301 TTCTTCAATGAACCTGAGAGCTGAGCAGACGCGCTGTCTATTACTG 350
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGGC.....AGCTTGACTACAGGCTCT..... 372
|||||

```

115 sAlaArgSerGlyAspTyrClySerGlySerTyrTyrAsnProArgTyrT 132
373 .....GACTCTGGGGCCAGGAGTCTCTGGTCACCGTC 405
132 yrTyrTyrTyrTyrMetAspValTrpGlyLysGlyThrLeuValThrVal 148
406 TCCTCA 411
149 SerSer 150
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OM of: US-09-019-441-4 to: Issued Patents\_AA:\* out\_format : pfs

Date: Sep 23, 2002 10:00 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-DB=Issued Patents_AA -QFMT=Fastan -SUFFIX=ra1 -GAPOP=12.000  
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1
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Search information block:

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Query: US-09-019-441-4  
Query length: 411  
Database: Issued Patents_AA:*  
Database sequences: 231628  
Database length: 24425594  
Search time (sec): 70.150000
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score\_list:

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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-99	+	508.00	971.40	1.1e-46	117
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/cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-259-372A-2	+	501.00	956.02	6.5e-46	141
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/cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-921-100-55	+	465.00	886.68	4.7e-42	141

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; Patent No. 5419904  
; GENERAL INFORMATION:  
; APPLICANT: Irie, Reiko F  
; TITLE OF INVENTION: HUMAN B-LYMPHOBLASTOID CELL LINE  
; TITLE OF INVENTION: SECRETING ANTI-GANGLIOSIDE ANTIBODY  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Poms, Smith, Lande & Rose  
; STREET: 2029 Century Park East, Suite 3800  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: United States of America  
; ZIP: 90067  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WordPerfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/026,320A  
; FILING DATE: 26-FEB-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/609803  
; FILING DATE: 05-NOV-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Oldenkamp, David J  
; REGISTRATION NUMBER: 29421  
; REFERENCE/DOCKET NUMBER: 94268  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 3102771297  
; TELEFAX: 3102771297  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-026-320A-2
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Quality: 516.00 Length: 141  
Ratio: 4.195 Gaps: 2  
Percent Similarity: 87.234 Percent Identity: 72.340

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|||||  
17 GlnCysGluValGlnLeuLeuLeuAspSerGlyGlyLeuValGlnProG 34  
|||||  
101 GGGGTCCTTCAGACTCTGGTGGCAGCGCTCCGGGTCAGGTTACCTTC 150  
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34 LysGlyCysLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
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49 SerSerCysalaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GTGGGTCTCAGCTATTAGTAGTGTGTGATCCACATGTCACCACT 250
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65 utrpValSerAlaIleSerGlySerGlySerThrThrTyrrAlaAsps 82
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82 erValLysGlyArgPheThrIleSerArgAspLysSerLysAsnThrLeu 98
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99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrrCy 115
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; Patent No. 6096878
; GENERAL INFORMATION:

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; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; NUMBER OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154

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; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-545-809A-99

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Percent Similarity: 94.068      Percent Identity: 81.356
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17 IGLnCysGlnValGlnLeuValGluSerGlyGlyLeuValLysProG 34
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101 GGGGGTCCCTGAGACTCTGTGCGCAGCCCTCCGGGTTTCAGGTTTCACCTTC 150
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; Patent No. 6210671
; GENERAL INFORMATION:
; APPLICANT: CO, Man Sung
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/579,378A
; FILING DATE: 27-DEC-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/160,074
; FILING DATE: 30-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,946
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95112895.8

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; FILING DATE: 17-AUG-1995
; PRIOR APPLICATION NUMBER: EP 95114696.8
; FILING DATE: 19-SEP-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschultz, Joe O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 11823-002220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 135 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-579-378A-20

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65 uTrpValAlaSerIleSerThrGlyGlySer...ThrTyTrpProAsps 81
251 CCGTGAAGGGAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
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81 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnThrLeu 97
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98 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyTrpCy 114
351 TGGCAGCTTGACTACAGGG...TCTGACTCTCTGGGGCGAGGAGTCCTGG 397
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114 sAlaArgAspTyArgGlyTyTrpPheAspTyTrpGlyGlnGlyThrLeuV 131
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; Sequence 2, Application US/08259372A
; Patent No. 5565354
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
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; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-259-372A-2
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alignment_scores:
  Quality: 501.00      Length: 143
  Ratio: 4.107        Gaps: 3
  Percent Similarity: 85.315  Percent Identity: 72.028

alignment_block:
US-09-019-441-4 x US-08-259-372A-2 ..
Align seg 1/1 to: US-08-259-372A-2 from: 1 to: 141
1 ATGGAGTTGGGTCAGCTGGGTTTCCCTCTCTCTTTTGAAGGCTG 50
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1 MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17
51 CCAGTGTGAGGTGACGTGGTGGAGTCTGGGGGGCGCTTGCAAGCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
101 GGGGTCCCTCAGACTCTGGTGGCGAGGCTCCGGGTTTCAGGTTACCTTC 150
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```

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34  lyArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGACCTGGGTCGCCAGGCTCCAGGCAGGGGCTGGA 200
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49  SerArgTyGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuG1 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201 GTGGTCTCAGCTATTAGTAGTAGTGGTATGCCACATGTTAGCGACAGCT 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65  utrpValAlaValIleSerTyAspGlySerAsnLysTrpTyAlaAsps 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 CCGTGAAGGCGAGATTCACATCTCCAGAGAGAACGCCAACACACACTG 300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82  erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 TTTCTTCAATCAACAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99  PheLeuGlnMetHisSerLeuArgAlaAlaAspThrGlyValTyTyrcy 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
351 TCGG.....AGCTTGACTACAGGCTCTGACTCC.....TGGG 382
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
115 saLaLysAspGlnLeuTyPheGlySerGlnSerProGlyHisTyTrpv 132
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
383 GCCAGGGAGCTCTGTGCTACCGTCTCTCTCA 411
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 alGlnGlyThrLeuValThrValSerSer 141
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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seq\_name: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:US-08-468-671-2

seq\_documentation\_block:

; Sequence 2, Application US/08468671

; Patent No. 5648077

; GENERAL INFORMATION:

; APPLICANT: Ostberg, Lars G.

; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Center, Eighth Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,671

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 424

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/259,372

; FILING DATE: 14-JUN-1994

; APPLICATION NUMBER: US 07/871,426

; FILING DATE: 21-APR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/676,036

; FILING DATE: 27-MAR-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/538,796

; FILING DATE: 15-JUN-1990

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/192,754

; FILING DATE: 11-MAY-1988

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 06/925,196

; FILING DATE: 31-OCT-1986

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 06/904,517

; FILING DATE: 05-SEP-1986

; ATTORNEY/AGENT INFORMATION:

; ATTORNEY/AGENT INFORMATION:

```
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 141 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-468-671-2
```

alignment\_scores:

Quality: 501.00 Length: 143  
Ratio: 4.107 Caps: 3  
Percent Similarity: 85.315 Percent Identity: 72.028

alignment\_block:

US-09-019-441-4 x US-08-468-671-2 ..

Align seg 1/1 to: US-08-468-671-2 from: 1 to: 141

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    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1  MetGluPheGlyLeuSerTrpValPheLeuValAlaLeuLeuArgGlyVa 17
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
51  CCAGTGTGAGGTGCGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCCTG 100
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
17  GlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
101 GGGGTCTCTGAGACTCTGGTGGCGAGCTCCGGGTTTCAGGTTTCACCTTC 150
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
34  lyArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
151 AATRACTACTACATGAGCTGGTGGTCCGCCAGGCTCCAGGCAGGGGCTGGA 200
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49  SerArgTyGlyMetHisTrpValArgGlnAlaProGlyLysGlyLeuG1 65
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
201 GTGGTCTCAGCTATTAGTAGTAGTGGTATGCCACATGTTAGCGACAGCT 250
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
65  utrpValAlaValIleSerTyAspGlySerAsnLysTrpTyAlaAsps 82
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
251 CCGTGAAGGCGAGATTCACATCTCCAGAGAGAACGCCAACACACACTG 300
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
82  erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
301 TTTCTTCAATCAACAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
99  PheLeuGlnMetHisSerLeuArgAlaAlaAspThrGlyValTyTyrcy 115
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
351 TCGG.....AGCTTGACTACAGGCTCTGACTCC.....TGGG 382
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
115 saLaLysAspGlnLeuTyPheGlySerGlnSerProGlyHisTyTrpv 132
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
383 GCCAGGGAGCTCTGTGCTACCGTCTCTCTCA 411
    : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 alGlnGlyThrLeuValThrValSerSer 141
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seq\_name: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:US-08-259-372A-4

seq\_documentation\_block:

; Sequence 4, Application US/08259372A

; Patent No. 5565354

; GENERAL INFORMATION:

; APPLICANT: Ostberg, Lars G.

; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL

; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

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; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,372A
; FILING DATE: 14-JUN-1994
; CLASSIFICATION: 424
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-259-372A-4

alignment_scores:
    Quality: 499.00      Length: 137
    Ratio: 4.229         Gaps: 3
    Percent Similarity: 86.131      Percent Identity: 74.453

alignment_block:
US-09-019-441-4 x US-08-259-372A-4 ..
Align seg 1/1 to: US-08-259-372A-4 from: 1 to: 131

1 ATGGAGTTGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50
|||||
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa 17
|||||
51 CCAGTGTGAGTGTGAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
|||||
101 GGGGTCCTCCTGAGACTGTGTCGGCAGCTCCCGGTTTCAGTTTCACCTTC 150
|||||
34 lGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
|||||
151 AATAACTACTACATGAGTGGTCCGCGAGGCTCCAGGCGAGGCGCTGGA 200
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49 SerArgTrpAspMetTyrTrpValArgGlnAlaThrGlyLysGlyLeuG1 65
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201 GTGGTCTCAGCTATTAGTAGTAGTGTGATCCCATGCTAGCAGACT 250
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65 utrPvalSerAlaIleGlyProThrGlyAsp...ThrTyrAlaAsps 81
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81 erVallySGlyArgPheThrIleSerArgGluAsnAlaLysAsnSerLeu 97
|||||
301 TTCTTCAATGAACAGCCCTGAGAGCTGAGGACACAGCGCTGTCTATTACTG 350
|||||
98 TyrLeuThrMetAsnGlyLeuArgAlaGlyAspThrAlaValTyrTyC 114
|||||
351 TGCAGCTTGCAGTACAGGGTCTGACTCCTCGGGCCAGGAGTCTGTGCTCA 400
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114 sAla.....ArgAspLeuGluLeuTrpGlyGlnGlyThrLeuValT 128
|||||
401 CCCTCTCTCTCA 411
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128 hrValSerSer 131

seq_name: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:US-08-468-671-4

seq_documentation_block:
; Sequence 4, Application US/08468671
; Patent No. 5648077
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
; TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,671
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/259,372
; FILING DATE: 14-JUN-1994
; APPLICATION NUMBER: US 07/871,426
; FILING DATE: 21-APR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,036
; FILING DATE: 27-MAR-1991
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/538,796
; FILING DATE: 15-JUN-1990
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/192,754
; FILING DATE: 11-MAY-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 06/925,196
; FILING DATE: 31-OCT-1986
; APPLICATION DATA:
; APPLICATION NUMBER: US 06/904,517
; FILING DATE: 05-SEP-1986
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-50-7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
```

```
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-468-671-4

alignment_scores:
  Quality: 499.00      Length: 137
  Ratio: 4.229        Gaps: 3
Percent Similarity: 86.131 Percent Identity: 74.453

alignment_block:
US-09-019-441-4 x US-08-468-671-4

Align seg 1/1 to: US-08-468-671-4 from: 1 to: 131

1 ATGGAGTTTGGGCTGAGCTGGGTTTCCCTGTCTCTTTTGAAGGTGT 50
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa 17
51 CCAGTGTGAGTGCAGCTGCTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCCTCTGAGACTCTGGTCGCGAGCTCCGGGTTCAAGTTACCTTC 150
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACATGAGTCTGGTCGCGAGCTCCAGGCGGAGGCTCGA 200
49 SerArgTyrAspMetTyrTrpValargGlnAlaThrGlyLysGlyLeuG 65
201 GTGGGCTCTACGTATTAGTAGTGGTGGTATCCACATGGTACGAGACT 250
65 utrPValSerAlaIleGlyProThrGlyAsp...ThrTyrTyrAlaAspS 81
251 CCGTCAAGGCGAGATTACCATCTCCAGAGACAGCCCAACACACACTG 300
81 erValLysGlyArgPheThrIleSerArgGluAsnAlaLysAsnSerLeu 97
301 TTTCTTCAATCAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTG 350
98 TyrLeuThrMetAsnGlyLeuArgAlaGlyAspThrAlaValTyrTyrCy 114
351 TGGGAGCTTGACTACAGGCTCTGACTCTCGTGGGCGGAGGAGTCTGTG 400
114 sAla.....ArgAspLeuGluLeuTrpGlyGlnGlyThrLeuValT 128
401 CCGTCTCTCTCA*411
128 hrValSerSer 131

seq_name: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:US-08-129-930B-96

seq_documentation_block:
; Sequence 96, Application US/08129930B
; Patent No. 5804187
; GENERAL INFORMATION:
; APPLICANT: do Couto Dr., Fernando J.R.
; APPLICANT: Ceriani Dr., Roberto L.
; APPLICANT: Peterson Dr., Jerry A.
; APPLICANT: Padlan Dr., Eduardo A.
; TITLE OF INVENTION: Analogue Peptides With Broad
; TITLE OF INVENTION: Carcinoma Specificity, and Kit and
; TITLE OF INVENTION: Diagnostic Vaccination, and
; TITLE OF INVENTION: Therapeutic Methods
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: V. AMZEL & ASSOC.

; STREET: 2055 No. 5804187th Broadway, Suite 201
; CITY: Walnut Creek
; STATE: California
; COUNTRY: USA
; ZIP: 94596
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS 5.0
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/129,930B
; FILING DATE: September 30, 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel Ph.D., Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: CRFCC-008A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 521-1333
; TELEFAX: (510) 521-3541
; TELEX: n.a.
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-129-930B-96

alignment_scores:
  Quality: 496.00      Length: 141
  Ratio: 4.066        Gaps: 2
Percent Similarity: 86.525 Percent Identity: 70.213

alignment_block:
US-09-019-441-4 x US-08-129-930B-96

Align seg 1/1 to: US-08-129-930B-96 from: 1 to: 139

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1 MetaspPheGlyLeuSerLeuValPheLeuValLeuLeuLysGlyVa 17
51 CCAGTGTGAGTGCAGCTGCTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
17 lGlnCysGluValGlnMetValGluSerGlyGlyLeuValGlnProG 34
101 GGGGTCCTCTGAGACTCTGGTCGCGAGCTCCGGGTTCAAGTTACCTTC 150
34 lYgLYSerLeuArgLeuSerCysAlaAlaSerGly.....PheAlaPhe 48
151 AATAACTACTACATGAGTCTGGTCGCGAGCTCCAGGCGGAGGCTCGA 200
49 SerSerTyrAlaMetSerTrpValargGlnAlaProGlyLysGlyLeuG 65
201 GTGGGTCCTACGTATTAGTAGTGGTGGTATCCACATGGTACGAGACT 250
65 utrPValAlaGluIleSerSerGlyGlyAsnTyrAlaTyrTyrGlnAsp 82
251 CCGTGAAGGCGAGATTCAACATCTCCAGAGAGAACGCCAACACACTG 300
82 hrValThrGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAATCAACAGCTGAGAGCTGAGGACAGGCTGTCTATTACTG 350
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
351 TGGGAGCTTGACTACAGGCTCTGACTCC.....TGGGGCGCAGG 388
115 sAlaArgGluAspTyrGlyIleProAlaTrpPheAlaTyrTrpGlyGlnG 132
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; MOLECULE TYPE: peptide  
; US-08-976-288A-96

alignment\_scores:  
  Quality: 496.00           Length: 141  
  Ratio: 4.066             Gaps: 2  
Percent Similarity: 86.525   Percent Identity: 70.213

alignment\_block:

US-09-019-441-4 x US-08-976-288A-96   ..

Align seg 1/1 to: US-08-976-288A-96 from: 1 to: 139

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1 ATGGAGTTGGCTGAGCTGGGTTTCTCTGTCTCTTTTGAAGGTCT 50
|||||
1 MetAspPheGlyLeuSerLeuValPheLeuValLeuLeuLysGlyVa 17
|||||
51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 lGlnCysGluValGlnMetValGlnSerGlyGlyLeuValGlnProG 34
|||||
101 GGGGTCTCTGAGACTCTGGTGGCGAGCTCCGGGTTCAGGTTCACCTTC 150
|||||
34 lYglySerLeuArgLeuSerCysAlaAlaSerGly.....PheAlaPhe 48
|||||
151 AATACTACTACATGAGCTGGTGGTCCGCCAGGCTCCAGGCGGCTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65
|||||
201 GTGGTCTCAGCTATTAGTAGTGGTGATCCACATGGTACGAGACT 250
|||||
65 utrpValAlaGluIleSerSerGlyAsnTyrAlaTyrTyrGlnAspT 82
|||||
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAGAACCCCAACACACTG 300
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82 hrValThrGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||
301 TTCTTCAATGAACAGCTGAGAGCTGAGACAGGCTGCTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||
351 TGGCAGCTTGACTACAGGCTGTGACTCC.....TGGGGCCAGG 388
|||||
115 sAlaArgGluAspTyrGlyIleProAlaTrpPheAlaTyrTrpGlyGlnG 132
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389 GAGTCTGCTCAGCTCTCTCTCA 411
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132 lYthrLeuValThrValSerSer 139
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seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-545-809A-109

seq\_documentation\_block:

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; Sequence 109, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545.809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 109:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 117 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-545-809A-109
```

alignment\_scores:  
  Quality: 492.00           Length: 118  
  Ratio: 4.514             Gaps: 1  
Percent Similarity: 92.373   Percent Identity: 79.661

alignment\_block:

US-09-019-441-4 x US-08-545-809A-109   ..

Align seg 1/1 to: US-08-545-809A-109 from: 1 to: 117

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1 ATGGAGTTGGGCTGAGCTGGGTTTCTCTGTCTCTTTTGAAGGTCT 50
|||||
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaLysIleLysGlyVa 17
|||||
51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
|||||
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34
|||||
101 GGGGTCTCTGAGACTCTGGTGGCGAGCTCCGGGTTCAGGTTCACCTTC 150
|||||
34 lYglySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
|||||
151 AATACTACTACATGAGCTGGTGGTCCGCCAGGCTCCAGGCGGCTGGA 200
|||||
49 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65
|||||
201 GTGGGTCTCAGCTATTAGTAGTGGTGATCCACATGGTACGAGACT 250
|||||
65 utrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAsps 82
|||||
251 CCGTGAAGGCGAGATTTCACCATCTCCAGAGAGAACCCCAACACACTG 300
|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
|||||
301 TTCTTCAATGAACAGCTGAGAGCTGAGACAGGCTGCTCTATTACTG 350
|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115
|||||
351 TGGC 354
|||||
115 sAla 116
```

seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-545-809A-107

seq\_documentation\_block:

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; Sequence 107, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
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99 TyrLeuGlnMetAsnSerLeuArgAlaIguAspThrAlavalrrYrcY l15

351 TGCG 354
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115 sala 116

seq_name: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:US-08-545-809A-l30

seq_documentation_block:
; Sequence 130, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
```

```

? NAME: Freeman, John W.
? REGISTRATION NUMBER: 29,066
? REFERENCE/DOCKET NUMBER: 06501/004001
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 617-542-5070
? TELEFAX: 617-542-8906
? TELEX: 200154
? INFORMATION FOR SEQ ID NO: 130:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 117 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-545-809A-130

alignment_scores:
    Quality: 481.00      Length: 118
    Ratio: 4.413        Gaps: 1
    Percent Similarity: 92.373    Percent Identity: 78.814

alignment_block:
    US-09-019-441-4 x US-08-545-809A-130    ..

Align seg 1/1 to: US-08-545-809A-130 from: 1 to: 117

1 ATGGAGTTGGGCTGACCTGGGTTTTCTTGTCTCTTTCAAAGGTCT 50
1 MetGluLeuGlyLeuCysTrpValPheLeuValAlaIleLeuGluGlyVa 17
51 CCAGTCTGAGGTGCAGCTGGTGGAGCTTGGGGCGGCTTGGCAAAGCCCTG 100
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
101 GGGGGTCCCTTGAGACTCTGGTGCGCAGCCTCGGGTTCAGGTTACACCTTC 150

```

```

alignment_scores:
  Quality: 481.00      Length: 118
  Ratio: 4.413         Gaps: 1
  Percent Similarity: 92.373  Percent Identity: 78.814

alignment_block:
  US-09-019-441-4 x US-08-545-809A-130  ..

Align seg 1/1 to: US-08-545-809A-130 from: 1 to: 117

1  ATGGAGTTTGGGCTGACCTGGGTTTTCCTTGTTCTCTTTGCAAGGTCGT 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1  MetGluLeuGlyLeuCysTrpValPheLeuValAlaIleLeuGluGlyVa 17

51  CCAAGTCGTAGGTCACAGCTGGTGAGCTGTGGGGGGCGCTTGGCAAAGCCG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17  lGlnCysGluVallGlnLeuValGlnSerGlyGlyLeuValGlnProG 34

101  GGGGGTCCCTGAGACTCTGGTCGCAGCGCTCCGGGTTTCAGGTTACACCTTC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

34 lyGlySerLeuArgLeuSerCysAlaIleSerGly.....PheThrPhe 48  
151 AATACTACTACATGGAGTGGGTCCGCCAGGCTCCAGGCAGGGCGGTGA 200  
:::||||| ||||:::|||||:::|||||:::|||||:::|||||  
49 SerTyrSerMetAsnTrpValArgInlAlaprogLyLysGlyLeuGl 65  
:::||||| |||||:::|||||:::|||||:::|||||:::|||||  
201 GTGGGTCACGATTAGTAGTAGTGNGATCCCACATGTCAGCGACACT 250  
||||||| ||||| ||||| ||||| ::|||::|||::|||  
65 uTpValSerTyrlleSerSerSerSerThrIleTyrTyrrAlaAsps 82  
||||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
251 CCTGAAGGGCAGATTCAACCATCTCCAGAGAAGCGCCAAACAACACTGC 300  
erValLysGlyArgPheThrIleSerArgaspaSnAlaLysAsnSerLeu 98  
TTTCTTTCAATCAACAGCCTCAGAGCTCAGGCACAGCGCTGCTATTACTG 350  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrcy 115  
  
351 TCGC 354  
||||  
115 sala 116

seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-545-809A-95

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: seq_documentation_block:
: Sequence 95, Application US/08545809A
: Patent No. 6036878
: GENERAL INFORMATION:
: APPLICANT: Honjo, Tasuku
: APPLICANT: Matsuda, Fumihiro
: TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
: TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
: NUMBER OF SEQUENCES: 145
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.

```

COMMENTS: 05  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,809A  
FILING DATE: 27-MAR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP93/006603  
FILING DATE: 10-MAY-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 06501/004001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-542-5070  
TELEFAX: 617-542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 95:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 117 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-545-809A-95

alignment_scores:		
Quality	478.00	Length: 118
Ratio	4.268	Gaps: 1
Percent Similarity	94.915	Percent Identity: 76.271

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alignment_block:
US-09-019-441-4 x US-08-545-809A-95      ..
Align seg 1/1 to: US-08-545-809A-95 from: 1 to: 117

1 ATGAGATTGGCGTACCTGGGTTCCTTGTTCCCTCTTTTGAAGGTGT 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 MetGluLeuGlyLeuSerTrpValPheLeuValAlaIleLeuGluGlyVa 17
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 CCAGTGTGAGGTGCAGCTGTGGAGTCTGGGGCGGCTTGGCAAAACCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GGGGGTCCCCTGAGACTCTGTGTCCAGCCCTCCGGGTTCAGGTTACCTTC 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 AATAACTACTACATGGACTGGTCCGCCAGGCTCCAGGCAGGGGGCTGA 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerTrpMetSerTrpValArgGlnAlaProGlyLysGlyLeuGl 65
|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 GTGGGTCTCACGTATTAGTAGTGGTGTATCCACATGGTACGCAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 uTrpValAlaAsnIleLysGlnAspGlySerGluLysTyrTyrValAspS 82
|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 CCGTGAAGGCAGATTACCATCTCCAGAGAGAAGCCCAACAACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 TTTCTTCAAATGAACAGCCTGAGAGCTGAGGACAGCGCTGCTATTACTG 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrcy 115
|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 TGCG 354
|||||
115 sAla 116

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seq\_name: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:US-08-545-809A-106

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seq_documentation_block:
; Sequence 106, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,809A
; FILING DATE: 27-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP93/00603
; FILING DATE: 10-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Freeman, John W.
; REGISTRATION NUMBER: 29,066
; REFERENCE/DOCKET NUMBER: 06501/004001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906

```

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; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 117 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
; US-08-545-809A-106

alignment_scores:
  Quality: 478.00      Length: 118
  Ratio: 4.426        Gaps: 1
  Percent Similarity: 91.525  Percent Identity: 77.966

alignment_block:
  US-09-019-441-4 x US-08-545-809A-106  ..
  Align seg 1/1 to: US-08-545-809A-106  from: 1 to: 117

1 ATGGAGTTTGGCTGAGCTGGGTTTCCTCTCTCTTTTGAAGGTGT 50
  |||||||
1 MetGluPheGlyLeuSerTrpValPheLeuValAlaIleLeuLysGlyVa 17
51 CCAGTGTGAGCTGAGCTGGTGGAGTCTGGGGCGGCTTGCCAAAGCCTG 100
  |||||||
17 LglnCysGluValGlnLeuValGluSerGlyGlyValValArgProG 34
101 GGGGTCCTCCTGAGACTCTGTGTCGCAGCTCCGGGTTTCAGGTTACCTTC 150
  |||||||
34 LylGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACAGCTGGCTGGCCAGGCTCCAGGGCAGGGGCTGGA 200
  |||||||
49 AspAspTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
201 GTGGTCTCACGTTATTAGTACTAGTGTGATCCACATGTTACGCAGACT 250
  |||||||
65 utrpValSerGlyIleAsnTrpAsnGlyGlySerThrGlyTyrAlaAsps 82
251 CCGTGAAGGGCAGATTACCATCTCCAGAGAGAACGCCAACACACACTG 300
  |||||||
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98
301 TTTCTTCAATGACAGCTGAGAGCTGAGGACAGCGGCTGTCTATTACTG 350
  |||||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaLeuTyrHisCy 115
351 TCGG 354
  ||||
115 sala 116
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/SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA1993.DAT.AA38161	+ 497.50	848.73	2.1e
/SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA1994.DAT.AA52833	+ 496.00	849.07	2.7e
/SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA1995.DAT.AA70471	+ 496.00	849.07	2.7e
/SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA1992.DAT.AA20057	+ 496.00	837.98	3.3e
/SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA2000.DAT.AA32406	+ 494.50	846.56	3.8e
seq name: /SIDSI/gcdata/hold-geneseq/geneseq-emb1/AA1998.DAT.AA70380			

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seq_documentation_block:
ID   AAW70380 standard; Protein; 137 AA.
XX
XX   AAW70380;
XX
XX   18-NOV-1998 (first entry)
DT
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KW	allergic rhinitis; conjunctivitis; autoimmune hemolytic anaemia
XX	
OS	Macaca fascicularis
XX	
FH	Key
FT	Location/Qualifiers
FT	1..19
FT	Protein
FT	/note= "Signal peptide"
FT	20..137
FT	Protein

score_list:	Sequence	Strd Orig	zScore	EScore	Len	! Documentation
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.AA070380 +		731.00	1252.85	9.0e-62	
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	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		540.00	911.51	2.1e-43	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		534.00	907.19	7.2e-43	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		534.00	905.68	7.2e-43	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		530.50	899.16	1.6e-42	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		528.00	903.22	3.8e-42	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		526.50	894.16	2.4e-42	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		523.50	895.09	6.6e-42	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		522.50	892.05	8.4e-42	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		516.50	875.52	3.5e-41	
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	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		515.00	881.83	4.2e-41	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		515.00	881.83	4.2e-41	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		515.00	881.83	4.2e-41	
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	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		510.00	872.86	1.3e-40	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		508.00	871.23	1.9e-40	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		507.00	856.83	3.0e-40	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		505.00	864.27	3.8e-40	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		505.00	855.36	4.4e-40	
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	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		501.00	846.84	1.1e-39	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		500.00	855.68	1.1e-39	
	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		499.00	854.75	1.4e-39	
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	/SDSI1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AA070380 +		497.50	851.32	2.0e-39	

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FT	Binding-site	120..126	
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XX			
PN	WO9837099-A1.		
XX			
XX	27-AUG-1998.		
XX			
XX	17-FEB-1998;	98WO-US02253.	
XX			
XX	05-FEB-1998;	98US-0803085.	
PR	20-FEB-1997;	97US-0803085.	
XX			
XX	(IDEC-) IDEC PHARM CORP.		
PA	(SEKG) SEIKAGAKU CORP.		
PI			
XX	Kloetzer WS, Nakamura T, Reff ME;		
DR	WPI; 1998-467495/40.		
DR	N-PSDB; AAV33310.		
XX			
PT	New anti-human CD23 monoclonal antibody - used for inhibiting Ig		
PT	expression to treat or prevent allergic, inflammatory and		
PT	auto:immune conditions		
XX			
XX	Example 1; Pages 108-110; 146pp; English.		
XX			
CC	The present sequence represents the heavy chain variable region		
CC	primate monoclonal antibody anti-human CD23 5E8. The invention		
CC	provides primate monoclonal antibodies which specifically bind h		
CC	CD23, the low affinity receptor for IgE (FcεRI/CD23), and compr		
CC	either of a human gamma-1 or human gamma-3 constant region that		
CC	to human Fc gamma receptors and inhibits IgE expression. The mo		
CC	antibodies of the invention are claimed to be useful for inhibit		
CC	induced IgE production for treating or preventing allergic, infl		
CC	and autoimmune conditions e.g. allergic rhinitis conjunctivitis,		
CC	auto:immune haemolytic anaemia, etc.		
XX			
XX	Sequence 137 AA;		





seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT-AAU14320  
seq\_documentation\_block:  
ID AAU14320 standard; Protein; 313 AA.  
XX AAU14320;  
XX  
XX  
XX 24-OCT-2001 (first entry)  
XX  
XX  
XX Human novel protein #191.  
XX  
XX Human: novel protein; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
OS Homo sapiens.  
XX  
XX WO200155437-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-US02623.  
XX  
XX 25-JAN-2000; 2000US-0491404.  
XX  
XX (HYSE-) HYSEQ INC.  
XX  
XX Tang YT, Liu C, Drmanac RT;  
XX  
XX WPI; 2001-451939/48.  
XX  
XX DR N-PSDB; AAS22625.  
XX  
XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX  
XX Example 4; Page 630-631; 894pp; English.  
XX  
XX The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicite an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
XX The present sequence represents a protein of the invention.  
XX  
XX Sequence 313 AA;

alignment\_scores:  
Quality: 538.50 Length: 148

Ratio: 4.343 Gaps: 2  
Percent Similarity: 83.784 Percent Identity: 72.297  
alignment\_block:  
US-09-019-441-4 x AAU14320 ..  
Align seg 1/1 to: AAU14320 from: 1 to: 313  
1 ATGAGAGTTTGGGTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50  
|||||  
42 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 58  
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCGTG 100  
58 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 75  
101 GGGGGTCCCTGAGACTCTGGTGGCGCAGCTCCGGGTTTCAGGTTCCACCTTC 150  
75 lGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 89  
151 AATAACTACTACATGAGCTGGTCCGCCAGGCTCCAGGGCAGGGCTGGA 200  
: : : : :  
90 SerSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 106  
201 GTGGTCTCAGCTATTAGTAGTAGTGTGATCCCATGTTACGACACT 250  
|||||  
106 uTrpValSerAlaIleSerGlySerGlySerThrTyrTyrAlaAspS 123  
251 CCGTGAAGGCGAGATTCCACCATCTCCAGAGAGAACGCCAACACACACTG 300  
|||||  
123 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 139  
301 TTTCTTCAATGAACAGCCTGAGAGCTGAGGACACGGCTGTCTATTACTG 350  
: : : : :  
140 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 156  
351 TGCAGAGCTTGACTACAGG..... 369  
156 sAlaLysSerHisProGlyTyrTyrTyrAspSerSerGlyTyrSerTyrT 173  
370 ..TCTGACTCTCTGGGCGCAGGAGTCTGGTCCACCGTCTCCTCA 411  
|||  
173 yrPheAspTyrTrpGlyGlnGlyThrLeuValThrValSerSer 187  
seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT-AAU14225  
seq\_documentation\_block:  
ID AAU14225 standard; Protein; 307 AA.  
XX  
XX AC AAU14225;  
XX  
XX DT 24-OCT-2001 (first entry)  
XX  
XX DE Human novel protein #96.  
XX  
XX Human: novel protein; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
XX OS Homo sapiens.  
XX  
XX PN WO200155437-A2.  
XX  
XX PD 02-AUG-2001.  
XX  
XX PF 25-JAN-2001; 2001WO-US02623.  
XX  
XX PR 25-JAN-2000; 2000US-0491404.  
XX

PA (HYSE-) HYSEQ INC.  
PI Tang YT, Liu C, Drmanac RT;  
XX WPI: 2001-451939/48.  
DR N-PSDB; AAS22530.  
XX  
PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX  
PS Example 4; Page 575; 894pp; English.  
XX  
CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicite an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.  
XX  
SQ Sequence 307 AA;

alignment\_scores:  
Quality: 534.00 Length: 137  
Ratio: 4.341 Gaps: 1  
Percent Similarity: 89.781 Percent Identity: 75.912

alignment\_block:  
US-09-019-441-4 x AAU14225 ..  
Align seg 1/1 to: AAU14225 from: 1 to: 307  
1 ATGGAGTTGGCTGAGCTGGGTTTCTCTTCTCTCTTTTGAAGGTGT 50  
1 MetGluPheGlyLeuSerTrpPheLeuValAlaIleLeuLysGlyVa 17  
51 CCAGTGTGAGGTGAGCTGGTGGAGTCTGGGGGGCTTGGCAAGCGCT 100  
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTGTGGTGGCGACGCTCCGGGTTTCAGGTTCACTTC 150  
34 lGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGAGTGGTGGTCCGACGCTCCAGGGCAGGGCTGGA 200  
49 SerSerPheSerMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGGTTCACGATTATAGTAGTGTGTATCCACATGATCGCAGACT 250  
65 uTrpValSerSerIleSerGlySerGlyThrThrThrTyrrAlaAsp 82  
251 -CCGTGAGGCGCATTCACCATCTCCAGAGAGAACGCCAACACACTG 300

82 erVallysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTCTTTCAAAATGAACAGCCTGAGAGCTGAGAGCAGCGCTGTCTATTACTG 350  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrrTyrcy 115  
351 TCGGAGCTTGACTACAGGCTCTGACTCTCTGGGGCCAGGAGTCTCTGGTCA 400  
115 salalysPheProPheProTyrrPheAspTyrrTrpGlyGlnGlyThrLeuValT 132  
401 CCGTCTCTCTCA 411  
132 hrValSerSer 135  
seq\_name: /SIDS1/gcgdata/hold-geneseg/genesegp-emb1/AA2001.DAT:AAU14228  
seq\_documentation\_block:  
ID AAU14228 standard; Protein; 363 AA.  
XX  
AC AAU14228;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE Human novel protein #99.  
XX  
KW Human; novel protein; Antianemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200155437-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-US02623.  
XX  
PR 25-JAN-2000; 2000US-0491404.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Liu C, Drmanac RT;  
XX  
DR WPI: 2001-451939/48.  
DR N-PSDB; AAS22533.  
XX  
PT Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX  
PS Example 4; Page 577; 894pp; English.  
XX  
CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicite an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a

CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
XX The present sequence represents a protein of the invention.

XX Sequence 363 AA;

alignment\_scores:  
Quality: 534.00 Length: 137  
Ratio: 4.341 Gaps: 1  
Percent Similarity: 89.781 Percent Identity: 75.912

alignment\_block:

US-09-019-441-4 x AAU14228

Align seg 1/1 to: AAU14228 from: 1 to: 363

1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50  
|||||  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17  
51 CCAGTGTGAGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCTG 100  
|||||  
17 LGInCysGluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTCTGTGGCGGCCCTCCGGTTTCAGGTTCCACTTC 150  
|||||  
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGAGTGGTGGTCCGAGGCTCCAGGCGAGGGCTGGA 200  
|||||  
49 SerSerPheSerMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65  
201 GTGGGTCTCAGTATTAGTAGTAGTGTGTGATCCACATGTTGACGACT 250  
|||||  
65 utrPValSerSerIleSerGlySerGlyThrThrTrpValAlaAsps 82  
251 CCGTGAAGGCGAGATTCCACATCTCCAGAGAACGCCCAACACACTG 300  
|||||  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98  
301 TTTCTTCAATGAACAGCTGAGAGCTGAGAGACACGGCTGTCTATTACTG 350  
:::|||||  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115  
351 TGCGAGCTTGACTACAGGCTGACTCTGGGCGCAGGAGCTCTGGTCA 400  
|||||  
115 sAlaLysProPheProTyrPheAspTyrTrpGlyGlnGlyThrLeuValT 132  
401 CCGTCTCTCTCA 411  
|||||  
132 hrValSerSer 135

seq\_name: /STDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.AAM24101

seq\_documentation\_block:

ID AAM24101 standard; Protein; 384 AA.

XX AC AAM24101;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1626.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;  
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;  
KW diagnostics; forensic test; gene mapping; genetic disorder;  
KW biodiversity; gene therapy; nutrition.

OS Homo sapiens.  
XX WO200154477-A2.  
XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-US02687.  
XX 25-JAN-2000; 2000US-0491404.  
PR 17-JUL-2000; 2000US-0617746.  
PR 03-AUG-2000; 2000US-0631451.  
PR 15-SEP-2000; 2000US-0663870.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;  
PI Cao Y, Drmanac RA, Zhang J, Werhman T;  
XX WPI: 2001-476164/51.  
DR N-PSDB; AAH98760.  
XX Isolated polypeptide for treatment of diseases, diagnostics, raising  
PT antibodies and research use -  
XX Claim 20; Page 1102-1103; 1275pp; English.  
XX The present invention provides the protein and coding sequences of novel  
CC proteins from a variety of organisms, including human, dog, cat, horse,  
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea  
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)  
CC from the organism of interest. They can be used in diagnostics,  
CC forensics, gene mapping, identification of mutations, to assess  
CC biodiversity and for nutritional purposes. The present sequence is a  
CC protein of the invention.  
XX Sequence 384 AA;

alignment\_scores:

Quality: 530.50 Length: 154

Ratio: 4.278 Gaps: 2

Percent Similarity: 80.519 Percent Identity: 68.831

alignment\_block:

US-09-019-441-4 x AAM24101

Align seg 1/1 to: AAM24101 from: 1 to: 384

1 ATGGAGTTTGGGCTGAGCTGGGTTTCTCTGTTCTCTTTTGAAGGTGT 50  
|||||  
1 MetGluPheGlyLeuSerTrpLeuPheLeuValAlaIleLeuLysGlyVa 17  
51 CCAGTGTGAGTGCAGCTGTGGAGTCTGGGGGGCTTGGCAAGCTG 100  
|||||  
17 LGInCysGluValGlnLeuValGluSerGlyGlyLeuValGlnProG 34  
101 GGGGGTCCCTGAGACTCTGTGGCGCACCTCCGGGTTTCAGGTTCCACTTC 150  
|||||  
34 lyGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGAGTGGTCCGCGCAGGCTCCAGGCGAGGGCTGGA 200  
|||||  
49 SerSerTrpAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65  
201 GTGGGTCTCAGTATTAGTAGTAGTGTGTGATCCACATGTTGACGACT 250  
|||||  
65 utrPValSerGlyIleGlySerGlySerGlySerThrTrpValAlaAsps 82  
251 CCGTGAAGGCGAGATTCCACATCTCCAGAGAACGCCCAACACACTG 300  
|||||  
82 erValLysGlyArgPheThrIleSerArgAspAsnSerGlnAsnThrLeu 98  
301 TTTCTTCAATGAACAGCTGAGAGCTGAGAGACACGGCTGTCTATTACTG 350

99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115  
351 TCGGAGC  
115 sAlaLysSerHisProAlaTyrTyrTyrGlySerGlySerTyrSerSerH 132  
358 .....TTGACTACAGGGTCTGACTCCTGGGGCCAGGAGTCCTGTC 399  
132 sTyrTyrTyrTyrTyrGlyMetAspValTyrGlyGlnGlyThrThrVal 148  
400 ACCGCTCCTCA 411  
149 ThrValSerSer 152

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAB99111

seq\_documentation\_block:  
ID AAB99111 standard; Protein; 152 AA.

XX AAB99111;  
XX 22-AUG-2001 (first entry)  
XX Human protein SEQ ID 4.  
XX Human; antiarthritic; cardiant; monoclonal antibody; keloid; arthritis;  
KW Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;  
KW signal transduction inhibition; tissue fibrosis; atherosclerosis.  
XX OS Homo sapiens.  
XX WO200136642-A1.  
XX 25-MAY-2001.  
XX 17-NOV-2000; 2000WO-JP08129.  
XX 18-NOV-1999; 99JP-0328681.  
XX 08-NOV-2000; 2000JP-0340216.  
XX (NISB ) JAPAN TOBACCO INC.  
XX Sakamoto S, Kamada M;  
XX WPI; 2001-343825/36.  
XX N-PSDB; AAH41153.  
XX Human monoclonal antibodies recognizing human TGF-beta II receptor,  
PT useful for treating TGF-beta associated diseases such as tissue  
PT fibrosis -  
XX Claim 10; Page 94-95; 118pp; Japanese.  
XX The present invention relates to novel human monoclonal antibodies. The  
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II  
CC receptor, resulting in the inhibition of the signal transduction of human  
CC TGF-beta into cells. The antibodies can be used for the prevention and  
CC treatment of diseases associated with the production of TGF-beta, such as  
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,  
CC atherosclerosis, atopy, keloid and arthritis. The present sequence was  
CC used in the present invention.  
XX Sequence 152 AA;

alignment\_scores:  
Quality: 528.00 Length: 137  
Ratio: 4.328 Gaps: 1  
Percent Similarity: 89.051 Percent Identity: 75.912  
alignment\_block:  
US-09-019-441-4 x AAB99111 ..

Align seg 1/1 to: AAB99111 from: 1 to: 152

1 ATGAGTTTGGCTCAGCTGGGTTTTCCTCTCTCTTTTGAAGGTGT 50  
1 MetGluLeuGlyLeuArgTyrPheLeuValAlaIleLeuGluGlyVa 17  
51 CCAGTGTGAGCTGCAGCTGTGGAGTCTGGGGGGGCTTGGCAAAGCCTG 100  
17 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 34  
101 GGGGTCCTCAGACTCTGTGTCGCGAGCCTCCGGGTTTCAGGTTACCTTC 150  
34 lGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATAACTACTACATGGAGCTGGTCCGCGAGCTCCAGGCGAGGGGCTGA 200  
49 SerSerPheSerMetAsnTyrPheValArgGlnAlaProGlyLysGlyLeuG 65  
201 GTGGTCTCAGCTATTAGTAGTGTGTGATCCACATGTTACGACACT 250  
65 utrpValSerSerIleSerSerSerSerSerTyrIleTyrTyrThrAsp 82  
251 CCGTGAAGGCGAGATTCCATCTCCAGAGAGAACGCCAACACACACTG 300  
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysAsnSerLeu 98  
301 TTTCTTCAATGAACGCTGAGAGCTGAGACACGCTGTCTATTACTG 350  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCy 115  
351 TGCAGGCTTCACTACAGGCTGTGACTCTCTGGGGCCAGGAGTCTCTGTC 400  
115 sAlaArgGlyTyrTyrPheAspTyrTyrGlyGlnGlyThrLeuValT 132  
401 CCGTCTCCTCA 411  
132 hrValSerSer 135

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT:AAU14227

seq\_documentation\_block:  
ID AAU14227 standard; Protein; 312 AA.

XX AAU14227;  
XX 24-OCT-2001 (first entry)  
XX Human novel protein #98.  
XX Human; novel protein; Antianaemic; osteopathic; antiinflammatory;  
KW immunomodulatory; cytostatic; neuroprotective; vulnery; nootropic;  
KW anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiviral;  
KW antibacterial; antiallergic; dermatological; haemostatic; antiasthmatic;  
KW thrombolytic; immunogen; antibody; gene therapy; neurological disorder;  
KW Parkinson's disease; inflammatory disorder; cancer; asthma; osteoporosis;  
KW tissue regeneration; immune disorder.  
XX Homo sapiens.  
XX WO200155437-A2.  
XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-US02623.  
XX 25-JAN-2000; 2000US-0491404.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT;  
XX WPI; 2001-451939/48.

N-PSDB; AAS22532.

Isolated polypeptides useful for treating anti-inflammatory diseases,  
nervous system disorders, and for regenerating bone and cartilage -

Example 4; Page 576-577; 894pp; English.

The invention relates to polynucleotides encoding novel human  
proteins or their active domains. The polypeptides, polynucleotides and  
antibodies raised against the polypeptides are used in a method of  
treatment of a mammal and prevention of disorders caused by the aberrant  
protein expression or activity. The polypeptides can be used as  
molecular weight markers, food supplements, and in antibody production.  
The polypeptides are used to identify compounds which bind to the  
polypeptides. Polynucleotides of the invention are used as probes and  
primers, for sequencing, for chromosome or gene mapping, in the  
production of recombinant proteins, and in generating anti-sense DNA or  
RNA and in gene therapy. Polypeptides of the invention can be used to  
target drugs to a tumour, in assays to determine biological activity, to  
raise antibodies/elicit an immune response, to determine quantitative  
protein levels, as tissue markers, and to isolate receptors or ligands.  
Polypeptides of the invention may also be useful in treating platelet  
disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
ligament and/or nerve tissue, wound healing, treating burns, promoting  
the proliferation, differentiation and survival of stem cells, as a  
contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
fungal infection or from autoimmunity, cancer, allergy, asthma,  
graft-versus-host disease, eczema, haemophilia, thrombosis,

DR N-PSDB; AAS22532.

XX Isolated polypeptides useful for treating anti-inflammatory diseases,  
PT nervous system disorders, and for regenerating bone and cartilage -  
XX Example 4; Page 576-577; 894pp; English.

CC The invention relates to polynucleotides encoding novel human  
CC proteins or their active domains. The polypeptides, polynucleotides and  
CC antibodies raised against the polypeptides are used in a method of  
CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicit an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host disease, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.

XX Sequence 312 AA;

alignment\_scores:

	Quality:	Length:
US-09-019-441-4 x AAU14227 ..	526.50	142
	Ratio: 4.179	Gaps: 3
	Percent Similarity: 88.732	Percent Identity: 72.535

alignment\_block:  
US-09-019-441-4 x AAU14227 ..

Align seg 1/1 to: AAU14227 from: 1 to: 312

	1	ATGGAGTTTGGCGTAGCTGTTTCCTTGCTCCTTTTGAAGGTGT	50
1	MetGlupheGlyLeuSerTrpPleuPheuValalaileuLysGlyIva	17	
51	CCAGTGTGACGTCAGCTGTGTGGAGTCTGGGGCGGTGGCAAGCGTG	100	
17	IgLnCysgluValGlnLeuLeuGluSerGlyGlyLeuValGlnProG	34	
101	GGGGTCCCTGAGACTCTGGTGCCGACGCCCTCCGGGTTCAGTTTCACCTTC	150	
34	LyGlyserLeuArgLeuSerCysalaalathrGly.....PheThrPhe	48	
151	AATACTACTACATGGAGTGGTCCGCCAGGCCTCCAGCGGAGGGCTGGA	200	
49	SerSerrYAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG	65	
201	GTGGTCTCACATTAGTACTGTGTGATCCCATGTCAGCAGACT	250	
65	utrPvalSerGluillelleSerSerGlyGlyThrThyTyrrAlaAsps	82	
251	CCGTGAAGGGGAGATTACCATTCTCCAGAGAGACGCCAACAACACTG	300	
82	erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu	98	
301	TTCCTTAATGAACAGCTGAGAGCTGAGACACACAGCTGCTGTATTACTG	350	
99	TYeuGlnMetAsngLYMetArgAlagLUasPhyrAlaleTVtyrvCy	115	

CC anti-inflammatory diseases, nervous system disorders, and infection.  
XX The present sequence represents a protein of the invention.  
SQ Sequence 159 AA;

alignment\_scores:  
Quality: 523.50 Length: 142  
Ratio: 4.122 Gaps: 3  
Percent Similarity: 89.437 Percent Identity: 71.831

alignment\_block:  
US-09-019-441-4 x AAU14226 ..

Align seg 1/1 to: AAU14226 from: 1 to: 159

1 ATGGAGTTGGCTGAGCTGGGTTTCTCTCTCTTTGAAAGGTGT 50  
|||||  
1 MetGluPheGlyLeuSerTrpLeuValAlaLeuLysGlyVa 17  
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTG 100  
|||||  
17 lGlnCysGluValGlnLeuLeuGluSerGlyGlyGlyLeuValGlnProG 34  
101 GGGGTCCTCAGACTCTGGTCCGCGAGCTCCGGGTTGAGTTACCTTC 150  
|||||  
34 lGlySerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48  
151 AATACTACTACATGAGCTGGGTCGGCAGGCTCCAGGCGAGGGCTGGA 200  
|||||  
49 AspSerTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuAs 65  
201 GTGGTCTCAGTATTAGTAGTGGTGATCCACATGGTACGAGACT 250  
|||||  
65 pTrpValSerAlaValSerGlyGlyGlySerThrTyrTyrAlaAspS 82  
251 CGGTGAAGGAGATTACCATCTCCAGAGAGAGAGCCCAACACACTG 300  
|||||  
82 erValLysGlyArgPheThrIleSerArgAspAsnAlaLysSerThrMet 98  
301 TTTCTCAATGAACAGCTGAGAGCTGAGGACGAGCTGTCTATTACTG 350  
|||||  
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaMetTyrTyCy 115  
351 TCGG.....ACCTTGACTACAGGTCT...GACTCCTGGGGCC 385  
|||||  
115 sAlaLysAspAsnTyrAspPheTrpSerGlyThrPheAspTyrTrpGlyG 132  
386 AGGAGTCTCCTGCTCAGCTCCTCTCA 411  
132 lGlyThrLeuValThrValSerSer 140

seq\_name: /SIDS1/gcdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AAW03726

seq\_documentation\_block:  
ID AAW03726 standard; Protein; 184 AA.

AC AAW03726;

DT 02-APR-1997 (first entry)

DE Humanised Mab 39-1.106 heavy chain variable region.

XX Heavy chain; variable region; murine; mouse; anti-human; disease;  
KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
KW diagnosis; inhibition; B-cell; activation; treatment; disorder;  
KW immune; autoimmune; allergic response; organ rejection; drug;  
KW graft versus host; cell imaging; tumour; targeted; delivery;  
XX targeted; humanised.

OS Mus\_musculus.

XX Key Location/Qualifiers

FT

FT Misc-difference 13 /note= "corresponding codon TCA"  
FT Misc-difference 23 /note= "corresponding codon TAA"  
XX  
PN WO9623071-A2.  
XX  
XX 01-AUG-1996. 96WO-US01119.  
XX 26-JAN-1996;  
XX 26-JAN-1995; 95US-0379057.  
XX  
PA (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;  
PI Harris LJ, Hollenbaugh D, Sladak AW;  
XX  
DR WPI; 1996-362694/36.  
DR N-PSDB; AAT36025.  
XX  
XX Monoclonal antibodies specific for different epitope(s) on human  
PT gp39 - used for inhibiting B cell activation and for the diagnosis  
PT of various disorders, e.g. cancer, psoriasis etc..  
XX  
XX Example 13; Fig 18; 167pp; English.

CC The present sequence is the heavy chain variable region of the  
CC humanised murine anti-human glycoprotein (gp) 39 monoclonal  
CC antibody (MAB) 39-1.106. The MAB may be useful for diagnosing  
CC disease states, inhibiting B-cell activation and for treating  
CC immunological disorders, e.g. autoimmune disorders, allergic  
CC responses, organ rejection and graft versus host disease. It may  
CC also be used for imaging cells which express gp39 on their surface,  
CC e.g. tumour cells, and to target therapeutic agents to such cells.  
CC The MAB inhibits the CD40/gp39 interaction, therefore limiting both  
CC prim. and sec. responses to T-cell dependent antigens and Ab prodn.  
CC specific to these antigens. A typical compsn. for intramuscular  
CC injection pref. contains 50 mg of MAB in 1 ml of sterile buffered  
CC water.

SQ Sequence 184 AA;

alignment\_scores:

Quality: 522.50 Length: 141  
Ratio: 4.318 Gaps: 3

Percent Similarity: 85.816 Percent Identity: 75.177

alignment\_block:

US-09-019-441-4 x AAW03726 ..

Align seg 1/1 to: AAW03726 from: 1 to: 184

1 ATGGAGTTGGCTGAGCTGGGTTTCTCTCTCTTTGAAAGGTGT 50  
|||||  
38 MetGluLeuGlyLeuArgTrpValPheLeuValAlaIleLeuGlyVa 54  
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGGGGCTTGGCAAGCCTG 100  
|||||  
54 lGlnCysGluValGlnLeuValGluSerGlyGlyLeuValLysProG 71  
101 GGGGTCCTCAGACTCTGGTCCGCGAGCTCCGGGTTTCAGGTTACCTTC 150  
|||||  
71 lGlySerLeuArgLeuSerCysAlaThrSerGly.....PheThrPhe 85  
151 AATACTACTACATGAGTCTGGTCCGCGAGCTCCAGGCGAGGGCTGGA 200  
|||||  
86 AsnAsnTyrAlaMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 102  
201 GTGGTCTCAGTATTAGTAGTGTGATCCACATGCTGTCAGCAGACT 250  
|||||  
102 utrPValAlaSerIle...SerSerGlyAspSerIleTyrIleAlaAspS 118







CC or an antibody (preferably monoclonal) or antibody fragment.  
 CC recognising pThrP. The antibody is preferably humanised or chimeric.  
 CC The present invention also describes a humanised antibody prepared  
 CC by hybridoma 23-57-137-1 (FERM BP-5631). The composition is used for  
 CC the treatment of cachexia arising in connection with diseases such as  
 CC cancer, thereby improving the quality of life of the patient. The  
 CC present sequence represents a human antibody heavy chain from the  
 CC present invention.

XX Sequence 137 AA;

alignment\_scores:  
 Quality: 515.00 Length: 139  
 Ratio: 4.221 Gaps: 2  
 Percent Similarity: 87.770 Percent Identity: 74.101

alignment\_block:

US-09-019-441-4 x AAW89635 ..

Align seg 1/1 to: AAW89635 from: 1 to: 137

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1 ATGGAGTTGGCGCTGAGCTGGGTTTTCTCTTCTCTTTTGAAGGTGT 50
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa 17
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
101 GGGGTCCTCAGACTCTGGTGGCGCAGCTCCGGGTTTCAGGTTTCACCTTC 150
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATACTACTACATGGAGTGGTGGTCCGCGAGCTCCAGGCGAGGCGTGA 200
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGTCTCAGCTATTAGTAGTAGTGGTATCCACATGTCACGAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 utrPValAlaThrIleSerSerGlyGlySerTyrTyrTyrProAspS 82
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTG 350
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGCAGCTTGACTACAGGTCT.....GACTCCTGGGGCCAGGAGTCC 394
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132
395 TGGTCACCGTCTCCTCA 411
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
132 euValThrValSerSer 137

```

seq\_name: /STDs1/gcdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AA77514

seq\_documentation\_block:

ID AAY77514 standard; Protein; 137 AA.

XX AAY77514;

AC AAY77514;

XX 26-APR-2000 (first entry)

XX Peptide encoded by DNA seq ID No: 58.

XX Hypocalcemic crisis; parathyroid hormone related peptide; pThrP; tumour.

XX Homo sapiens.

XX

PN WO200000219-A1.

XX 06-JAN-2000.

XX 25-JUN-1999; 99WO-JP03433.

XX 26-JUN-1998; 98JP-0180143.

XX (CHUS ) CHUGAI SEIYAKU KK.

XX Sato K, Tsunenari T;

XX WPI: 2000-117115/10.

XX N-PSDB; AAZ58914.

PT Treatment of hypercalcemic crisis with a substance inhibiting binding  
 of parathyroid hormone related peptide to its receptor

XX Example 4; Page 98-99; 120pp; Japanese.

XX The invention relates to a method of treatment of hypercalcemic crisis.  
 CC A composition for the treatment of hypercalcemic crisis contains as  
 CC active component a substance which inhibits the binding of parathyroid  
 CC hormone related peptide (pThrP) to its receptor. The inhibitor is used  
 CC for the treatment of hypercalcemic crisis, such as that associated with  
 CC a malignant tumour.

XX Sequence 137 AA;

alignment\_scores:

Quality: 515.00 Length: 139  
 Ratio: 4.221 Gaps: 2  
 Percent Similarity: 87.770 Percent Identity: 74.101

alignment\_block:

US-09-019-441-4 x AAY77514 ..

Align seg 1/1 to: AAY77514 from: 1 to: 137

```

1 ATGGAGTTGGCGCTGAGCTGGGTTTTCTCTTCTCTTTTGAAGGTGT 50
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuArgGlyVa 17
51 CCAGTGTGAGTGCAGCTGGTGGAGTCTGGGGCGGCTGGCAAGCCTG 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 lGlnCysGlnValGlnLeuValGluSerGlyGlyValValGlnProG 34
101 GGGGTCCTCAGACTCTGGTGGCGCAGCTCCGGGTTTCAGGTTTCACCTTC 150
||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
34 lYArgSerLeuArgLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATACTACTACATGGAGTGGTGGTCCGCGAGCTCCAGGCGAGGCGTGA 200
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuG 65
201 GTGGTCTCAGCTATTAGTAGTAGTGGTATCCACATGTCACGAGACT 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
65 utrPValAlaThrIleSerSerGlyGlySerTyrTyrTyrProAspS 82
251 CCGTGAAGGCGAGATTACCATCTCCAGAGAACGCCAACACACACTG 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAATGAACAGCTGAGAGCTGAGGACACGCTGTCTATTACTG 350
:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrCy 115
351 TGCAGCTTGACTACAGGTCT.....GACTCCTGGGGCCAGGAGTCC 394
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
115 sAlaArgGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132
395 TGGTCACCGTCTCCTCA 411
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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|||||
132 euValThrValSerSer 137
seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2001.DAT: AAG67112
seq_documentation_block:
ID   AAG67112 standard; Protein; 137 AA.
XX
AC   AAG67112;
XX
DT   13-NOV-2001 (first entry)
XX
DE   Amino acid sequence of a human protein.
XX
KW   Tissue decomposition inhibitor; parathyroid hormone; cancer cachexia;
KW   septicemia; injury; muscular dystrophy; cytokine; interleukin-6;
KW   granulocyte colony stimulating factor; interleukin-11;
KW   leukemia inhibitory factor; weight loss.
XX
OS   Homo sapiens.
XX
FH   Key Location/Qualifiers
FT   Peptide 1..19 /note= "signal peptide"
FT   Protein 20..137 /note= "mature protein; this sequence given as sequence
FT   FT number 56 in the specification"
XX
PN   WO200164249-A1.
XX
PD   07-SEP-2001.
XX
PF   30-AUG-2000; 2000WO-JP05886.
XX
PR   28-FEB-2000; 2000JP-0052414.
XX
PA   (CHUS ) CHUGAI SEIYAKU KK.
XX
PI   Saito H, Tsunenari T, Onuma E, Sato K;
DR   WPI; 2001-550131/61.
DR   N-PSDB; AAH75115.
XX
PT   Tissue decomposition inhibitor that prevents parathyroid hormone
PT   associated proteins from binding to its receptor
XX
PS   Example 1; Page 107-108; 132pp; Japanese.
XX
CC   The specification describes a tissue decomposition inhibitor, which
CC   comprises a substance that inhibits peptides associated with
CC   parathyroid hormone (PTH) from binding with their receptor. The method
CC   is used to inhibit tissue decomposition caused by cancer cachexia,
CC   septicemia, heavy external injury or muscular dystrophy, and for
CC   treating patients with elevated cytokine (Interleukin-6, Granulocyte
CC   colony stimulating factor, Interleukin-11 and Leukemia inhibitory
CC   factor) levels. It may also be used for preventing weight loss caused
CC   by cancer cachexia. The present sequence represents a protein, which is
CC   used in the course of the invention.
XX
SQ   Sequence 137 AA;

alignment_scores:
Quality: 515.00 Length: 139
Ratio: 4.221 Gaps: 2
Percent Similarity: 87.770 Percent Identity: 74.101

alignment_block:
US-09-019-441-4 x AAG67112 ...
Align seg 1/1 to: AAG67112 from: 1 to: 137
1 ATGAGATTGGCTGAGCTGGGTTTCCTGTTCCTCTTTTGAAGGTGT 50

```

```

|||||
1 MetGlyPheGlyLeuSerTrpValPheLeuValAlaLeuLeuAargGlyVa 17
51 CCAGTGTGAGGTGCAGCTGGTGGAGTCTGGGGCGGCTTGGCAAGCCTG 100
17 IGLnCysGlnValGlnLeuValGluSerGlyGlyGlyValValGlnProG 34
101 GGGGTCCCTGAGACTCTGTGTCGCGCAGCCTCGGGTTTCAGGTTTCACCTTC 150
34 LArgSerLeuAargLeuSerCysAlaAlaSerGly.....PheThrPhe 48
151 AATAACTACTACGACTGGTGGTCCGCGCAGGCTCCAGGCGCAGGGCTGGA 200
49 SerSerTyrGlyMetSerTrpValArgGlnAlaProGlyLysGlyLeuG1 65
201 GTGGGTCTCACCTATTAGTAGTAGTGGTGATCCACATGCGTACGAGACT 250
65 uTrpValAlaThrIleSerSerGlyGlySerTyrThrTyrTyrProAsps 82
251 CCGTGAAGGGCAGATTCCACCATCTCCAGAGAGAGAGCCCAACACACTG 300
82 erValLysGlyArgPheThrIleSerArgAspAsnSerLysAsnThrLeu 98
301 TTTCTTCAANTGAACAGCCTGAGAGCTGAGGACACGCGCTGTCTATTACTG 350
99 TyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTy-Cy 115
351 TGCAGGCTTGACTACAGGGTCT.....GACTCCTGGGGCCAGGAGTCC 394
115 sAlaAargGlnThrThrMetThrTyrPheAlaTyrTrpGlyGlnGlyThrL 132
395 TGGTCACCGTCTCCTCA 411
132 euValThrValSerSer 137

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Date: Sep 23, 2002 10:06 AM  
About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

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seq\_documentation\_block:

ID AAW70377 standard; Protein; 130 AA.

AC AAW70377;

XX 18-NOV-1998 (first entry)

DT Anti-human CD23 6G5 monoclonal antibody light chain variable region.

DE Anti-human CD23 6G5 monoclonal antibody; light chain variable region;

KW human CD23; IgE; FcεRI/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.

OS Macaca fascicularis

XX Key Location/Qualifiers

FT Protein 1..19 /note= "Signal peptide"

FT Protein 20..130

FT Binding-site 42..55 /note= "anti-human CD23 6G5 light chain variable region"

FT Binding-site 71..77 /note= "CDR 1"

FT Binding-site 110..119 /note= "CDR 2"

FT Binding-site 110..119 /note= "CDR 3"

PN WO9837099-A1.

XX 27-AUG-1998.

XX 17-FEB-1998; 98WO-US02253.

XX 05-FEB-1998; 98US-0803085.

XX 20-FEB-1997; 97US-0803085.

PA (IDEC ) IDEC PHARM CORP.

PA (SEKG ) SEIKAGAKU CORP.

PI Klotz WS, Nakamura T, Reff ME;

XX WPI; 1998-467495/40.

DR N-PSDB; AAV33307.

XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE

XX expression to treat or prevent allergic, inflammatory and

XX auto-immune conditions

XX Example 1; Pages 102-104; 146pp: English.

XX The present sequence represents the light chain variable region of

XX primate monoclonal antibody anti-human CD23 6G5. The invention

XX provides primate monoclonal antibodies which specifically bind human

XX CD23, the low affinity receptor for IgE (FcεRI/CD23), and comprise

XX either of a human gamma-1 or human gamma-3 constant region that binds

XX to human Fc gamma receptors and inhibits IgE expression. The monoclonal

XX antibodies of the invention are claimed to be useful for inhibiting

XX induced IgE production for treating or preventing allergic, inflammatory

XX and autoimmune conditions e.g. allergic rhinitis conjunctivitis,

XX auto-immune haemolytic anaemia, etc.

XX Sequence 130 AA;

SQ

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alignment_scores:
  Quality: 686.00      Length: 130
  Ratio: 5.277         Gaps: 0
Percent Similarity: 100.000      Percent Identity: 100.000

alignment_block:
US-09-019-441-1 x AAW70377 ..
Align seg 1/1 to: AAW70377 from: 1 to: 130

1 ATGGCCTGGACTGCTCTCGTCACCTCCTCACTCAGGGCACAGGATC 50
|||||
1 MetAlaTrpThrLeuLeuLeuValThrLeuLeuThrGlnGlyThrGlyse 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCTCTGTCTGGTCTCCTG 100
|||||
17 rTrpAlaGlnSerAlaProThrGlnProProSerValSerGlySerProG 34
101 GACAGTCGGTCACCATCTCTCGTACCTGGAACCGGATGAGTGGTGT 150
|||||
34 LyGlnSerValThrIleSerCysThrGlyThrSerAspValGlyGly 50
151 TATAACTATGTCCTCTGGTACCAACACCGGCAAGCCCAAACT 200
|||||
51 TyrAsnTyrValSerTrpTyrGlnHisHisProGlyLysAlaProLysLe 67
201 CATGATTATGATGTCCTAAGCGGGCTCAGGGTCTCTGTATCGCTTCT 250
|||||
67 uMetIleTyrAspValAlaLysArgAlaSerGlyValSerAspArgPheS 84
251 CTGGCTCCAAGTCGGCAACACGCGCTCCTGACCATCTCTGGGCTCCAG 300
|||||
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301 GCTGAGGACGAGCTGATTATTACTGTGTTCATATACACACCTAGTAC 350
|||||
101 AlaGluAspGluAlaAspTyrTyrCysSerTyrThrThrSerSerth 117
351 TTTGTTATTTCGGAAGAGGACCGGTTGACCGTCTAGGT 390
|||||
117 rLeuLeuPheGlyArgGlyThrArgLeuThrValLeuGly 130

seq_name: /SIDSI/gc9data/hold-geneseq/geneseq-emb1/AA1993.DAT:AAAR31024

seq_documentation_block:
ID AAR31024 standard; Protein; 235 AA.
XX
AC AAR31024;
XX
DT 19-MAY-1993 (first entry)
XX
DE Antibody D light chain.
XX
KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Signal peptide"
FT Region 20..42
FT /label= FR1
FT Region 43..53
FT /label= CDR1
FT Region 54..68
FT /label= FR2
FT Region 69..75
FT /label= CDR2
FT Region 76..107
FT /label= FR3
```

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FT Region 108..116
FT /label= CDR3
FT Region 117..126
FT /label= FR4
FT Domain 127..234
FT /label= C lambda
XX
PN EP523949-A.
XX
PD 20-JAN-1993.
XX
PF 14-JUL-1992; 92EP-0306420.
XX
PR 15-JUL-1991; 91GB-0015284.
PR 01-AUG-1991; 91GB-0016594.
PR 23-MAR-1992; 92GB-0006284.
XX
PA (WELL ) WELLCOME FOUND LTD.
XX
PI Crowe JS, Lewis AP;
DR WPI; 1993-019951/03.
DR N-PSDB; AAQ35100.
XX
Prodn. of recombinant primate antibodies - useful for treating
infections caused by hepatitis A, B and C, herpes,
cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,
arthritis etc.
PT
PT Disclosure; Fig 3; 35pp; English.
PS
XX
The sequences given in AAR31023-24 represent the heavy and light chains
of Antibody D respectively. Antibody D is a monoclonal antibody which
was derived from peripheral blood lymphocytes from a hepatitis A virus
(HAV) sero positive patient. Antibody D is closely related in nature
to murine antibody B5B3. Total RNA was isolated from antibody D
expressing cells and polyadenylated RNA was extracted. These polyA
RNA's were used to prepare a cDNA library which was screened for human
kappa light (L) chains and two positive clones were detected.
CC Further heavy (H) chain clones were also isolated.
XX
SQ Sequence 235 AA;

alignment_scores:
  Quality: 569.00      Length: 130
  Ratio: 4.664         Gaps: 0
Percent Similarity: 93.846      Percent Identity: 82.308

alignment_block:
US-09-019-441-1 x AAR31024 ..
Align seg 1/1 to: AAR31024 from: 1 to: 235

1 ATGGCTGGACTGCTCTCGTCACCTCCTCACTCAGGGCACAGGATC 50
|||||
1 MetAlaTrpAlaLeuLeuLeuLeuThrLeuLeuThrGlnAspThrGlyse 17
51 CTGGGCTCAGTCTGCCCGGCTCAGCTCCTCTGTCTGGTCTCCTG 100
|||||
17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34
101 GACAGTCGGTCACCATCTCTCGTACCTGGAACCGGATGAGTGGTGT 150
|||||
34 LyGlnSerIleThrIleSerCysThrGlyThrAsnAsnAspValGlySer 50
151 TATAACTATGTCCTCTGGTACCAACACCGGCAAGCCCAAACT 200
|||||
51 TyrAsnLeuValSerTrpTyrGlnGlnHisProGlyLysAlaProLysII 67
201 CATGATTATGATGTCGTAAGCGGGCTCAGGGTCTCTGTATCGCTTCT 250
|||||
67 eMetIleTyrGluValSerLysArgProSerGlyValSerAsnArgPheS 84
```





For encoding the HSBF, useful for diagnosing, treating or preventing

omo sapiens.

OS Homo sapiens.





PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	
XX	(HYSE-) HYSEQ INC.
PA	
XX	Drmanac RT, Liu C, Tang YT;
XX	
XX	WPI: 2001-639362/73.
DR	N-PSDB; AAS83477.
XX	
XX	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
PT	
XX	Claim 20; SEQ ID NO 49649; 103pp; English.
XX	

US-09-019-441-1 X ABG19291

The invention relates to isolated polynucleotides

polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AB000010-AG30377 represent novel human diagnostic amino acid sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Sequence 235 AA:

Align seq 1/1 to: ABG19290 from: 1 to: 235

1 ATGGCCCTGGACTCTGCTCTCTCTGTCACCCCTCTCTACTCAGGGACAGGATC 50  
1 MetAlatrprhrLeuLeuPheLeuThrLeuLeuthrGlnGlythrGlySe 17  
51 CTGGGCTCAGTCTGCCCGGACTCAGCTCAGCTCCCTCTGTCTCTGGGTCTCCG 100  
17 rTPaAGlnSerAlaLeuThrGlnPrAlaSerValSerGlySerProG 34  
101 GACAGTCGGTACCATCTCTGCACTCGAACCCAGCGATGACGTTGGTGGT 150

101 GACAGTCCGGTCACCAATCTCTCTGCACCTGGAACACCGGATGACCGTTGGTGGT 150

34 lyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla 50

131 TATAACATATGTCTCTCGTGGTACCAACACACCCAGGCAAAAGCCCCCAAACT 200

51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe 67

201 CATGATTTATGATGTCGCTAAGCGGGCCTCAGGGGCTCTCTGATCGCTTCT 250

67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS 84

XX  
251 CTGGCTCCAAGTCTGGCAACACGGGCTTCCCTGACCATCTCTGGGCTCCAG 300  
XX

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|||||
84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100
301 GCTCAGCAGCAGGCTGATTACTGTTGTTTCATATACACACCTAGCAC 350
|||||
101 AlaGluaspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerth 117
351 TTTGTTATTCCGAGAGAGGAGCCCGTTGACCGTCTAGGT 390
|||||
117 rValValPheGlyGlyThrSerValThrValLeuGly 130
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seq\_name: /SDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:ABG22850

seq\_documentation\_block:

ID ABG22850 standard; Protein; 236 AA.

AC ABG22850;

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22841.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS87037.

XX New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX Claim 20; SEQ ID No 53209; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,  
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
CC and gene mapping, and in recombinant production of (II). The  
CC polynucleotides are also used in diagnostics as expressed sequence tags  
CC for identifying expressed genes. (I) is useful in gene therapy techniques  
CC to restore normal activity of (II) or to treat disease states involving  
CC (II). (II) is useful for generating antibodies against it, detecting or  
CC quantitating a polypeptide in tissue, as molecular weight markers and as  
CC a food supplement. (II) and its binding partners are useful in medical  
CC imaging of sites expressing (II). (I) and (II) are useful for treating  
CC disorders involving aberrant protein expression or biological activity.  
CC The polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. ABG0010-ABG30377 represent novel human  
CC diagnostic amino acid sequences of the invention.  
CC Note: The sequence data for this patent did not appear in the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence, 236 AA;

PI Drmanac RT, Liu C, Tang YT;

alignment\_scores:

Quality: 544.00 Length: 130

Ratio: 4.496 Gaps: 0

Percent Similarity: 93.077 Percent Identity: 78.462

alignment\_block:

US-09-019-441-1 x ABG22850 ..

Align seg 1/1 to: ABG22850 from: 1 to: 236

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|||||

1 MetAlaIrpThrLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlyse 17

51 CTGGGCTCAGTCTGCCCGACTCAGCCTCCCTCTGCTGCTGGGTCTCTG 100

|||||

17 rTPAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

101 GACAGTCGGTCACCATCTCTCTGACCTGGAACACGAGGATGAGTGGTGGT 150

|||||

34 LyGlnSerIleThrIleSerCysIleGlyThrSerSerAspIleGlyAla 50

151 TATAACTATGTCCTCTGTTACCAACACCCAGGCAAGCCCAAACT 200

|||||

51 TyrTyrPheValSerTrpTyrGlnGlnTyrProGlyLysAlaProLysLe 67

201 CATGATTATGATCTCGCTAAGCGGCTCAGGGGCTCTGATCGCTCTCT 250

|||||

67 uLeuIlePheAspValSerGlyArgProSerGlyIleSerSerArgPheS 84

251 CTGGCTCCAAAGTCTGGCAACACGCGCTCCCTGACCATCTCTGGGCTCCAG 300

|||||

84 erGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACACACCTAGCAC 350

|||||

101 AlaGluAspGluAlaAspTyrTyrCysAlaSerTyrAlaArgSerSerth 117

351 TTTGTTATTCCGAGAGAGGAGCCCGTTGACCGTCTAGGT 390

|||||

117 rValValPheGlyGlyThrSerValThrValLeuGly 130

seq\_name: /SDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:ABG12887

seq\_documentation\_block:

ID ABG12887 standard; Protein; 161 AA.

AC ABG12887;

DT 13-FEB-2002 (first entry)

XX Novel human diagnostic protein #12878.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

PI



```
98 CTGACAGTCGGTACCATCTCTGCACTGGAACACCGCATGACGTTGGT 147
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 roGlyGlnSerIleThrIleSerCysThrGlyThrSerSerAspIleGly 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
148 GGTATTAACATATGTCCTCTGGTACCACACACCGGCAAGCCCAAA 197
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 GlyTyrAsnTyrValSerTyrGlnGlnHisProGlyLysAlaProLy 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
198 ACTCATGATTATGATCTGCTCAAGCGGCTCAGGGGTCTCTGATCGCT 247
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 sLeuValIleTyrAlaValSerAsnArgProSerGlyValSerHisArgp 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
248 TCTCTGGCTCCAAGTCTGGCAACACCGGCTCCCTGACCATCTCTGGGCTC 297
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 heSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerGlyLeu 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
298 CAGCGTACGACGAGGCTGATTATTACTGTGTTCATATACACACAGTAG 347
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
101 GlnAlaGluAspGluAlaAspTyrTyrCysAsnSerAspAlaSerThrSe 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
348 CACTTTCTTATTTCGGAAGAGCGGCTGACGCTCTAGGT 390
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
117 rLysTrpValPheGlyGlyThrLysLeuThrValLeuGly 131
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:ABG19298

seq\_documentation\_block:

ID ABG19298 standard; Protein; 236 AA.

XX

AC ABG19298;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #19289.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US08631.

XX

PR 31-MAR-2000; 2000US-0540217.

XX

PR 23-AUG-2000; 2000US-0649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

PI WPI; 2001-639362/73.

XX

DR N-PSDB; AAS83485.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations

PT responsible for genetic disorders or other traits and to assess

PT biodiversity -

XX

PS Claim 20; SEQ ID No 49657; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving

CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as

CC a food supplement. (II) and its binding partners are useful in medical

CC imaging of sites expressing (II). (I) and (II) are useful for treating

CC disorders involving aberrant protein expression or biological activity.

CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations

CC responsible for genetic disorders or other traits to assess biodiversity

CC and to produce other types of data and products dependent on DNA and

CC amino acid sequences. ABG00010-ABG0377 represent novel human

CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed

CC specification, but was obtained in electronic format directly from WIPO

CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX

SQ Sequence 236 AA;

alignment\_scores:

Quality: 527.50 Length: 131

Ratio: 4.433 Gaps: 1

Percent Similarity: 90.840 Percent Identity: 77.099

alignment\_block:

US-09-019-441-1 x ABG19298 ..

Align seg 1/1 to: ABG19298 from: 1 to: 236

1 ATGGCCTGGACTCTGCTCCCTGTCACCCCTCTCACTCAGGCACAGGATC 50

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1 MetAlaTrpAlaLeuLeuPheLeuThrLeuLeuThrGlnGlyThrGlySe 17

51 CTGGGCTCAGTCTGCCCGGACTCAGCCTCCCTCTGTGTCGTGGGTCTCCTG 100

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

17 rTrpAlaGlnSerAlaLeuThrGlnProAlaSerValSerGlySerProG 34

101 GACAGTCGGTCACCATCTCCTGCACTGGAAACGACGATGACGTGGTGGT 150

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

34 lyGlnSerIleThrIleSerCysThrGlySerSerSerAspValGlyGly 50

151 TATAACTATCTCTCTGGTACCAACACACCCAGCAAGCCCAAGCCCAACT 200

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

51 TyrAsnTyrValSerTrpTyrGlnGlnHisProGlyLysAlaProLysLe 67

201 CATGATTTATGATGTCGTAAAGCGGCTCAGGGGTCTCTGATCGCTTCT 250

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

67 uileHisTyrGlyGlySerLysArgProSerArgValTyrAspArgPheS 84

251 CTGGCTCCAAGTCTGGCAACACCGCCTCCCTGACCATCTCTGGGCTCCAG 300

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

84 erGlySerMetSerAlaAsnThrAlaSerLeuThrIleSerGlyLeuGln 100

301 GCTGAGGACGAGGCTGATTATTACTGTGTTCATATACACACCATAGCAC 350

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

101 AlaAspAspGluAlaAspTyrTyrCysCysSerPheAlaGlySerSerAl 117

351 TTGTG...TTATTCGGAAGAGGAGCCGGTTGACCGTCTAGGT 390

|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

117 aLeuArgIlePheGlySerGlyThrArgValIleValIleGly 131

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:ABG19296

seq\_documentation\_block:

ID ABG19296 standard; Protein; 244 AA.

XX

XX

AC ABG19296;

XX

DT 18-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #19287.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.



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SQ Sequence 117 AA:

alignment_scores:
  Quality: 524.00      Length: 116
  Ratio: 4.764        Gaps: 0
  Percent Similarity: 94.828  Percent Identity: 84.483

alignment_block:
US-09-019-441-1 x AAG80206 ..

Align seg 1/1 to: AAG80206 from: 1 to: 117

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2 ThrGlySerTrpAlaGluLeuValThrGlnProAlaSerValSerGI 18
|||||
93 GTCTCTGGACAGTCGGTCACCATCTCCTGCCTGGAACCGAGCATGACG 142
|||||
18 ySerProGlyGlnSerIleThrIleSerCysThrGlyThrSerSerAspV 35
|||||
143 TTGGTGGTTATACATATGCTCTCTGTGTACCAACACACCCAGGCAAGCC 192
|||||
35 aGlyGlyTyrAsnTyrValSerTyrTrpArgHisProAlaLysAla 51
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193 CCCAAACTCATGATTATGATGTCGTAAAGCGGGCCTCAGGGGTCTCTGA 242
|||||
52 ProLysLeuMetIleTyrAspValSerAsnArgProSerGlyValSerAs 68
|||||
243 TCCTCTCTCTGGCTCCAAGTCTGGCAACACGGCCTCCCTGACCATCTCG 292
|||||
68 nArgPheSerGlySerLysSerGlyAsnThrAlaSerLeuThrIleSerG 85
|||||
293 GGCTCCAGGCTGAGGACGAGGCTGATTATTACTGTGTTTCATATACAAC 342
|||||
85 lLeuGlnAlaGluAspGluAlaAspIleTyrCysSerSerTyrThrSer 101
|||||
343 AGTAGCACTTTGTTATTCGGAAGAGGACCCGGTTGACCGTCTCCTAGGT 390
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102 SerSerThrLeuValPheGlyGlyGlyThrLysLeuThrValLeuGly 117
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seq_documentation_block:
; Sequence 639, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 639
; LENGTH: 205
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-639

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alignment_scores:
  Quality: 595.00      Length: 129
  Ratio: 4.917        Gaps: 0
  Percent Similarity: 93.798  Percent Identity: 89.922

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alignment_block:
US-09-019-441-3 x US-09-760-479-639
Align seg 1/1 to: US-09-760-479-639 from: 1 to: 205

```

```

1 ATGACATGAGGTCCCGCTCAGCTCCTGGGCTCCTCTGCTCGCT 50
|||||
6 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuPLe 22
|||||
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
22 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 39
|||||
101 CTGCATCTGTAGGGCAGAGTCACCATCTGTCAGGGGCAAGTCAGGAC 150
|||||
39 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnIle 55
|||||
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACCAGGAAAAGCTCTAA 200
|||||
56 IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 72
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201 GTCCTGATCTATGTCATCCAGTTGCAAGTGGGGTCCCATCAAGGT 250
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72 sPheLeuIleTyrGlyAlaSerSerLeuGlnSerGlyValProSerArgp 89
|||||
251 TCAGCGCAGTGTGTCGACAGAGTTCACTCTCACCCTCAGCAGCCTG 300
|||||
89 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 105
|||||
301 CAGCCTGAAGATTTTGGACTTATTACTGTCTACAGTTTATAGTACCCC 350
|||||
106 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrThrPr 122
|||||
351 TCAGAGTTCGGCCAGGACCAAGGTGGAATCAAA 387
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122 oProThrPheGlyGlnGlyThrLysLeuGluIleLys 134

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seq_documentation_block:
; Sequence 8, Application US/60113635
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Preeti Lal
; APPLICANT: Jennifer L. Hillman
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; APPLICANT: Leo Shih

```

```

; APPLICANT: Junming Yang
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0658 P
; CURRENT APPLICATION NUMBER: US/60/113,635
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3238787
US-60-113-635-8

```

```

alignment_scores:
  Quality: 594.50      Length: 130
  Ratio: 4.833        Gaps: 1
  Percent Similarity: 94.615  Percent Identity: 90.000

```

```

alignment_block:
US-09-019-441-3 x US-60-113-635-8
Align seg 1/1 to: US-60-113-635-8 from: 1 to: 237

```

```

1 ATGACATGAGGTCCCGCTCAGCTCCTGGGCTCCTCTGCTCGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuPLe 17
|||||
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
|||||
101 CTGCATCTGTAGGGCAGAGTCACCATCTGTCAGGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
|||||
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACCAGGAAAAGCTCTAA 200
|||||
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
|||||
201 GTCCTGATCTATGTCATCCAGTTGCAAGTGGGGTCCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
|||||
251 TCAGCGCAGTGTGTCGACAGAGTTCACTCTCACCCTCAGCAGCCTG 300
|||||
84 heSerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
|||||
301 CAGCCTGAAGATTTTGGACTTATTACTGTCTACAGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117
|||||
351 TCGG....ACGTCGGCCAGGACCAAGGTGGAATCAAA 387
|||||
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130

```

```
seq_name: /cgn2_6/ptodata/2/paa/US091_COMB.pap:US-09-195-853-1
```

```

seq_documentation_block:
; Sequence 1, Application US/09195853
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Neil C. Corley
; APPLICANT: Karl J. Guegler
; APPLICANT: Gina A. Gorgone
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; TITLE OF INVENTION: HUMAN ANTIGEN RECOGNITION PROTEINS
; FILE REFERENCE: PF-0643 us
; CURRENT APPLICATION NUMBER: US/09/195,853

```



```
; CURRENT FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 079785
US-09-195-853-1
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alignment_scores:
  Quality: 590.50      Length: 130
  Ratio: 4.801        Gaps: 1
  Percent Similarity: 94.615  Percent Identity: 89.231
```

```
alignment_block:
US-09-019-441-3 x US-09-195-853-1 ..
Align seg 1/1 to: US-09-195-853-1 from: 1 to: 237
```

```
1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTCGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17
51 CCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer 50
151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCCAGGAAAGCTCCTAA 200
|||||
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCCTCTGATCTATGTTCCATCCAGTTTGCAGGTTGCGGCTCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGGCAGTGTGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117
351 TCGG...ACGTTCCGCCAAGGACCAAGTGGAAATCAAA 387
|||||
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
```

```
seq_name: /cgn2_6/ptodata/2/paa/US091_COMB.pap:US-09-195-853-1
```

```
seq_documentation_block:
; Sequence 1, Application US/09195853A
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Neil C. Corley
; APPLICANT: Karl J. Guegler
; APPLICANT: Gina A. Gorgone
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; TITLE OF INVENTION: HUMAN ANTIGEN RECOGNITION PROTEINS
; FILE REFERENCE: PF-0643 us
; CURRENT APPLICATION NUMBER: US/09/195,853A
; CURRENT FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PERL Program
; SEQ ID NO 1
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```
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: 079785
US-09-195-853-1

alignment_scores:
  Quality: 590.50      Length: 130
  Ratio: 4.801        Gaps: 1
  Percent Similarity: 94.615  Percent Identity: 89.231

alignment_block:
US-09-019-441-3 x US-09-195-853-1 ..
Align seg 1/1 to: US-09-195-853-1 from: 1 to: 237

1 ATGGACATGAGGTCCCGCTCAGCTCCTGGGCTCCTTCTGCTCGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17
51 CCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
|||||
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaGlyGlnSer 50
151 ATTAGGTATTATTAAATTGGTATCAGCAGAAACCCAGGAAAGCTCCTAA 200
|||||
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCCTCTGATCTATGTTCCATCCAGTTTGCAGGTTGCGGCTCCATCAAGGT 250
|||||
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGGCAGTGTGACAGAGTTCACTCTCACCGTCAGCAGCGCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117
351 TCGG...ACGTTCCGCCAAGGACCAAGTGGAAATCAAA 387
|||||
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130
```

```
seq_name: /cgn2_6/ptodata/2/paa/US100_COMB.pap:US-10-038-591-52
```

```
seq_documentation_block:
; Sequence 52, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-038-591-52

## alignment\_scores:

Quality: 590.00 Length: 129  
Ratio: 4.876 Gaps: 0  
Percent Similarity: 93.798 Percent Identity: 90.698

## alignment\_block:

US-09-019-441-3 x US-10-038-591-52 ..

Align seg 1/1 to: US-10-038-591-52 from: 1 to: 236

```
1 ATGCACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGTCTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17
51 CCAGGTGCCAGATGTGACATCAGATGACCCAGTCCCATCTCCCTGT 100
:|||||
17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50
151 ATTAGGTATTATTAAATGGTATCAGCAGAAACCAGGAAAGCTCCTAA 200
|||||
51 IleArgAsnAspLeuGlyTrpTyrglnGlnLysProGlyLysAlaProLy 67
201 GCTCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGGT 250
|||||
67 sArgLeuIleTyrglnAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrglnGlnHisAsnSerTyPr 117
351 TCGGAGCTTCGGCCAGGGACCAAGTGGAAATCAAA 387
117 oTyrrThrPheGlyGlnGlyThrLysLeuGluIleLys 129
```

seq\_name: /cgn2\_6/ptodata/2/paa/US100\_COMB.pap:US-10-038-591-48

## seq\_documentation\_block:

```
; Sequence 48, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; FILE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; CURRENT APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-48
```

## alignment\_scores:

Quality: 588.00 Length: 129

Ratio: 4.860 Gaps: 0  
Percent Similarity: 93.798 Percent Identity: 89.922

## alignment\_block:

US-09-019-441-3 x US-10-038-591-48 ..

Align seg 1/1 to: US-10-038-591-48 from: 1 to: 236

```
1 ATGCACATGAGGTCCCGCTCAGCTCCTGGGGCTCCTTCTGTCTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17
51 CCAGGTGCCAGATGTGACATCAGATGACCCAGTCCCATCTCCCTGT 100
:|||||
17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34
101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50
151 ATTAGGTATTATTAAATGGTATCAGCAGAAACCAGGAAAGCTCCTAA 200
|||||
51 IleArgAsnAspLeuGlyTrpTyrglnGlnLysProGlyLysAlaProLy 67
201 GCTCTGATCTATGTCATCCAGTTTGCAGTGGGGTCCCATCAAGGT 250
|||||
67 sArgLeuIleTyrglnAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrglnGlnHisAsnSerTyPr 117
351 TCGGAGCTTCGGCCAGGGACCAAGTGGAAATCAAA 387
117 oTyrrThrPheGlyGlnGlyThrLysLeuGluIleLys 129
```

seq\_name: /cgn2\_6/ptodata/2/paa/US100\_COMB.pap:US-10-038-591-51

## seq\_documentation\_block:

```
; Sequence 51, Application US/10038591
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; FILE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; CURRENT APPLICATION NUMBER: US/10/038,591
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-51
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## alignment\_scores:

Quality: 584.00 Length: 128  
Ratio: 4.826 Gaps: 0  
Percent Similarity: 94.531 Percent Identity: 89.062

## alignment\_block:

US-09-019-441-3 x US-10-038-591-51 ..

Align seg 1/1 to: US-10-038-591-51 from: 1 to: 236

```
1 ATGGACATGAGGGTCCCGCTCAGCTCCTCGGGGCTCCTTCTGCTCTGGCT 50
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17
51 CCCAGGTGCCAGATGTGACATCCAGATGCCAGTCTCCATCTTCCCTGT 100
17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
101 CTGCATCTGTAGGGACAGAGTCCAGATCCAGTCCAGTCTCCATCTTCCCTGT 100
17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
34 erAlaSerValGlyAspArgValThrPheThrCysArgAlaSerGlnasp 50
151 ATTAGGTATTATTAAATTTGGTATCAGCAAGAACCCAGGAAAGCTCTAA 200
51 IleArgArgAspLeuGlyTyrThrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCCTCATCTATGTTGCATCCAGTTCGCAAGTGGGGTCCCATCAAGGT 250
67 sArgLeuIleTyrAlaAlaSerArgLeuGlnSerGlyValProSerArgP 84
251 TCAGCGCAGTGGATCTGGACAGAGTTCACCTCTCACCGTCAGCAGCTG 300
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCC 350
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnAsnTyrPr 117
351 TCGGACGTTCGGCCAAAGGACCAAGTGGAAATC 384
117 oArgThrPheGlyGlnGlyThrGluValGluIle 128
```

seq\_name: /cgn2\_6/ptodata/2/paa/us098\_comb.pep:US-09-859-053-30

seq\_documentation\_block:

```
; Sequence 30, Application US/09859053
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30
```

alignment\_scores:  
Quality: 582.00 Length: 129  
Ratio: 4.850 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 88.372

alignment\_block:

US-09-019-441-3 x US-09-859-053-30 ..

Align seg 1/1 to: US-09-859-053-30 from: 1 to: 236

```
1 ATGGACATGAGGGTCCCGCTCAGCTCCTCGGGGCTCCTTCTGCTCTGGCT 50
```

```
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17
51 CCCAGGTGCCAGATGTGACATCCAGATGCCAGTCTCCATCTTCCCTGT 100
17 eProGlySerArgCysAspIleGlnMetThrGlnSerProSerSerVals 34
101 CTGCATCTGTAGGGACAGAGTCCAGTCCAGTCTCCAGTCTCCAGGCAAGTCAGGAC 150
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50
151 ATTAGGTATTATTAAATTTGGTATCAGCAAGAACCCAGGAAAGCTCTAA 200
51 IleSerArgLeuLeuAlaThrTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCCTCATCTATGTTGCATCCAGTTCGCAAGTGGGGTCCCATCAAGGT 250
67 sLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSerArgP 84
251 TCAGCGCAGTGGATCTGGACAGAGTTCACCTCTCACCGTCAGCAGCTG 300
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTTGGCACTTATTACTGTCTACAGGTTTATAGTACCC 350
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnAlaAsnSerPhePr 117
351 TCGGACGTTCGGCCAAAGGACCAAGTGGAAATCAAA 387
117 oTrpThrPheGlyGlnGlyThrLysValGluIleLys 129
```

seq\_name: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pep:PCT-US01-18569-2296

seq\_documentation\_block:

```
; Sequence 2296, Application PC/TUS0118569
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA13PCT
; CURRENT APPLICATION NUMBER: PCT/US01/18569
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2296
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (2)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (99)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (119)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (140)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (146)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US01-18569-2296
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alignment\_scores:

Quality: 579.00 Length: 129  
Ratio: 4.825 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 87.597

alignment\_block:  
US-09-019-441-3 x PCT-US01-18569-2296 ..  
Align seg 1/1 to: PCT-US01-18569-2296 from: 1 to: 260  
1 ATGGACATGAGGTCCTCCCTCAGCTCTGGGGCTCTTCTGCTCTGGCT 50  
|||||  
25 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriple 41  
51 CCCAGTGCCACATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100  
| |||||  
41 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 58  
|||||  
101 CTGCATCTGTAGGGACAGATCACCATCAGTTCAGGGCAAGTCAGGAC 150  
|||||  
58 eAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 74  
|||||  
151 ATTAGGTATTATTTAAATGGTATCAGCAGAAACCCAGGAAAGCTCCTAA 200  
|||  
75 IleSerAsnTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 91  
201 GCTCCTGATCTATGTGTCATCAGTTTGCAGAGTGGGTCCCATCAAGT 250  
|||||  
91 sLeuLeuIleTyrAlaAlaSer\*\*\*LeuGlnSerGlyValProSerArgp 108  
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300  
|||||  
108 heSerGlySerGlySerGlyThrAspPheThr\*\*\*ThrIleSerSerLeu 124  
301 CAGCTGAAGATTGCGACTTATTTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
125 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrAspAsn\*\*\*Pr 141  
351 TCGGACGTTTCGCGCAAGGACCAAGTGGAAATCAAA 387  
| |||||  
141 oLeuThrPheGly\*\*\*GlyThrLysValGluIleLys 153  
seq\_name: /cgn2\_6/ptodata/2/paa/US098\_COMB.pep:US-09-834-366-17896  
seq\_documentation\_block:  
; Sequence 17896, Application US/09834366  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.052.REG  
; CURRENT APPLICATION NUMBER: US/09/834,366  
; PRIOR FILING DATE: 2001-04-13  
; PRIOR APPLICATION NUMBER: US 60/197,873  
; PRIOR FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17896  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -22...-1  
US-09-834-366-17896

alignment\_scores:  
Quality: 578.00 Length: 129  
Ratio: 4.817 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 86.822  
alignment\_block:  
US-09-019-441-3 x US-09-834-366-17896 ..

Align seg 1/1 to: US-09-834-366-17896 from: 1 to: 146  
1 ATGGACATGAGGTCCTCCCTCAGCTCTGGGGCTCTTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriple 17  
51 CCCAGTGCCACATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100  
| |||||  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34  
|||||  
101 CTGCATCTGTAGGGACAGATCACCATCAGTTCAGGGCAAGTCAGGAC 150  
|||||  
34 eAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnThr 50  
|||||  
151 ATTAGGTATTATTTAAATGGTATCAGCAGAAACCCAGGAAAGCTCCTAA 200  
|||  
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67  
201 GCTCCTGATCTATGTGTCATCAGTTTGCAGAGTGGGTCCCATCAAGT 250  
|||||  
67 sLeuLeuIleTyrAlaAlaThrAsnLeuGlnSerGlyValProSerArgp 84  
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCGTCAGCAGCCTG 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCTGAAGATTGCGACTTATTTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGluAspTyrAlaIleTyrTyrCysGlnGlnSerAspSerSerPr 117  
351 TCGGACGTTTCGCGCAAGGACCAAGTGGAAATCAAA 387  
| |||||  
117 oTyrThrPheGlyGlnGlyThrLysLeuGluIleLys 129  
seq\_name: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep:US-60-197-873-17896  
seq\_documentation\_block:  
; Sequence 17896, Application US/60197873  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; APPLICANT: Dumas Milne Edwards, Jean Baptiste  
; APPLICANT: Jobert, Severin  
; APPLICANT: Giordano, Jean-Yves  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: 81.US1.PRO  
; CURRENT APPLICATION NUMBER: US/60/197,873  
; CURRENT FILING DATE: 2000-04-18  
; NUMBER OF SEQ ID NOS: 52153  
; SOFTWARE: Patent.pm  
; SEQ ID NO 17896  
; LENGTH: 146  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: -22...-1  
US-60-197-873-17896

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Ratio: 4.817 Gaps: 0  
Percent Similarity: 93.023 Percent Identity: 86.822  
alignment\_block:  
US-09-019-441-3 x US-60-197-873-17896 ..  
Align seg 1/1 to: US-60-197-873-17896 from: 1 to: 146  
1 ATGGACATGAGGTCCTCCCTCAGCTCTGGGGCTCTTCTGCTCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTriple 17

51 CCCAGGTGCCAGATGTCACATCCAGATGACCCAGTCTCCATCTTCCTGT 100  
17 uAGGlyAlaAArgCysaspIleGlnMetThrGlnSerProSerSerLeuS 34  
101 CTGCATCTGTAGGGGACAGAGTCACCATCACTTGCAGGGCAAGTCAGGAC 150  
34 eAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnThr 50  
151 ATTAGGTATTATTTAAATTCGTATCATCAGCAAAACACAGGAAAAGCTCTTAA 200  
51 lIeSerSerTyLeuAsnTpyTyGlnGlnLysProGlyLysAlaProLy 67  
201 GCTCCTGATCTATGTCATCCAGTCAGTTTGCAGAGTGGGGTCCCATCAAGT 250  
67 sLeuLeuIleTyrAlaAlaThrAsnLeuGlnSerGlyValProSerArg 84  
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACTCTCACCCTCAGCAGCCGTG 300  
84 hEserGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTCAAGATTTTGGCGACTTATTACTGTCCTACAGCTTTATAGTACCCC 350  
101 GlnProGluAspTyAlaIleTyTyCysGlnGlnSerAspSerPr 117  
351 TCGGACGCTCGCGCAGGGACCAAGGTGGAAATCAA 387  
117 oTyThrPhedIyGlnGlyThrTyLeuGluIleLys 129

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seq_name: /cgn2_5/ptodata/2/paa/US60_COMB pep:US-60-113-635-11
seq_documentation_block:
; Sequence 11, Application US/60113635
; GENERAL INFORMATION:
; APPLICANT: Henry Yue
; APPLICANT: Y. Tom Tang
; APPLICANT: Preeti Lal
; APPLICANT: Jennifer L. Hillman
; APPLICANT: Jennifer L. Hillman
; APPLICANT: Mariah R. Baughn
; APPLICANT: Aina Lu
; APPLICANT: Leo Shi
; APPLICANT: Junming Yang
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY PROTEINS
; FILE REFERENCE: PF-0658 P
; CURRENT APPLICATION NUMBER: US/60/113,635
; CURRENT FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE: -
; OTHER INFORMATION: 3981428
US-60-113-635-11

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  Ratio: 4.701        Gaps: 1
  Percent Similarity: 93.846      Percent Identity: 86.154

alignment_block:
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Align seg 1/1 to: US-60-113-635-11 from: 1 to: 237

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1  ATGCACATAGAGGCCCCCGTTCAGCTCCTGGGGCTCCTTCTGCTCTGGCT 50
|||||
1  MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuLeuTrpLe 17
|||||
51  CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100
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17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
101 CTGCATCTCTAGGGACAGAGTCCACCATCCTTCGACGGCAGTCCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrMetThrCysArgAlaSerGlnSer 50
151 ATTAGGTATTATTAAATTGGTATCAGCAGAGAACCAGGAAAAGTCCTTAA 200
|||||
51 IleSerThrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProly 67
201 GCTCTCTGATCATGTGTGCATCCAGTTTCGAAAGTCGGGTCCCATCAAGT 250
|||||
67 sleuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGCGGAGTGGATCTCGGACAGAGATTTCACCTCTCACGCTCAGCAGCCTG 300
|||||
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTTCGGACTTATTACTGTCTACAGGTTTATAGTACCCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerPheAsnThrHi 117
351 TCGG...ACGTTTCGCCAGGACCAAGTCGGAAATCAAA 387
117 sMetTyrThrPheGlyGlnGlyThrArgLeuGluMetLys 130

seq_name: /cgn2_6/ptodata/2/paa/US097_COMB.pep:US-09-760-479-852

seq_documentation_block:
; Sequence 852, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760.479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALLM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 852
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; NAME/KEY: SITE
; LOCATION: (80)
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; NAME/KEY: SITE
; LOCATION: (84)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; NAME/KEY: SITE
; LOCATION: (111)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; NAME/KEY: SITE
; LOCATION: (127)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; NAME/KEY: SITE
; LOCATION: (128)
; OTHER INFORMATION: Xaa equals any of the naturally occurring
; US-09-760-479-852

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  Ratio: 4.773        Gaps: 0
  Percent Similarity: 92.248      Percent Identity: 86.047

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1 ATGGACATCAGGCTCCCGCTCAGCTCCCTGGGCTCTCTCTCTGGCT 50  
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14 MetAspMetArgValProIaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 30  
|||||  
51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGCTCTCCATCTCCCTGT 100  
|||||  
30 uArgGlyAlaAArgCysAspMetGlnMetThrGlnSerProSerSerLeu 47  
|||||  
101 CTGCATCTAGGGACAGAGTCACCATCCTTCAGTTCAGGCAAGTCAGGAC 150  
|||||  
47 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 63  
|||||  
151 ATTAGGTATTATTAAATTTGGTATCAGAGAAACCAGGAAAGCTCTCAA 200  
|||||  
64 IleSerAsn\*\*\*LeuAsnTrpGlnGlnProGlyLysAlaPro\*\* 80  
|||||  
201 GCTCTGATCTATGTTCATCAGTTTCAAGTGGGTCCCATCAAGGT 250  
|||||  
80 \*LeuLeuIle\*\*\*AlaAlaSerThrLeuGlnSerGlyValProSerArgp 97  
|||||  
251 TCAGGGCAGTGGATCTGGGACAGAGTTCATCTCACCCTCAGCAGCCTG 300  
|||||  
97 heSerGlySerGlySerGlyThrAspPheThrLeuThrIle\*\*\*CysLeu 113  
|||||  
301 CAGCTCTGAAGATTTGGCAGCTTATTACTCTACAGGTTTATAGTACCCC 350  
|||||  
114 GlnProGluAspPheAlaThrTyrCysGlnGlnAsn\*\*\*\*\*ThrPr 130  
|||||  
351 TCGGACGTTCCGCCCAAGGACCAAGGTGGAATCAAA 387  
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130 oArgThrPheGlyGlnGlyThrLysValGluIleLys 142

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seq\_documentation\_block:  
; Sequence 1, Application PC/TUS0108518  
; GENERAL INFORMATION:  
; APPLICANT: INCYTE GENOMICS, INC.  
; APPLICANT: YUE, Henry  
; APPLICANT: HILLMAN, Jennifer L.  
; TITLE OF INVENTION: BAUGHN, Mariah R.  
; FILE REFERENCE: PF-0765 PCT  
; CURRENT APPLICATION NUMBER: PCT/US01/08518  
; CURRENT FILING DATE: 2001-03-15  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PERL Program  
; SEQ ID NO 1  
; LENGTH: 241  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Incyte ID No: 6100311CD1  
PCT-US01-08518-1

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Percent Similarity: 89.552 Percent Identity: 83.582

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1 ATGGACATCAGGCTCCCGCTCAGCTCCCTGGGCTCTCTCTCTGGCT 50  
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1 MetAspMetArgValProIaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17

51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGCTCTCCATCTTCCCTGT 100  
|||||  
17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeu 34  
|||||  
101 CTGCATCTGTAGGGACAGAGTCACCATCCTTCAGTTCAGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50  
|||||  
151 ATTAGG.....TATTATTAAATTTGGTATCAGCAGAAACC 185  
|||||  
51 IleSerSerGlnSerIleGlySerTrpLeuAlaTrpTyrGlnGlnLysPr 67  
|||||  
186 AGGAAAGACTCTTAAGCTCCTCATCTATGTTCATCCAGTTTGCAGAGTG 235  
|||||  
67 oGlyLysAlaProLysLeuLeuIleTyrLysAlaSerSerLeuGluSerG 84  
|||||  
236 GGGTCCCATCAAGGTTTCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTC 285  
|||||  
84 LyValProSerArgPheSerGlySerGlyThrGluPheThrLeu 100  
|||||  
286 ACCGTTCAGCAGCTTCAGCCTGAAGATTTTGGCAGCTTATTACTGTCTACA 335  
|||||  
101 ThrIleSerSerLeuGlnProAspPheAlaThrTyrTyrCysGlnG 117  
|||||  
336 GGTTTATAGTACCCCTCGGACGTTTCGGCCCAAGGACCAAGGTGGAATCA 385  
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117 nTyrAsnAsnTyrProTrpThrPheGlyGlnGlyThrLysValGluIleL 134  
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386 AA 387  
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134 ys 134

OM of: US-09-019-441-3 to: A\_Geneseq\_032802.\* out\_format : pfs

Date: Sep 23, 2002 10:06 AM

About: Results were produced by the GenCore software, version 4.5,  
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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-O=/cgn2_1/USPTO_pool/US09019441/runat_23092002_095257_6281/app_query.fasta_1.1860  
-DB=A_Geneseq_032802 -OFMT=fastan -SUFFIX=rag -GAPOP=0.000  
-GAPEXT=4.000 -MINMATCH=0.100 -LOOPEXT=0.000 -LOOPEXT=0.000  
-GAPOP=4.500 -GAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500  
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=10.000 -YGAPEXT=0.500  
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=blossum62  
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR_SCORE=pct  
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09019441 -CGN1_1.175 -NCPU=6 -ICPU=3 -LONGLOG  
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Search information block:

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Query length: 387  
Database: A_Geneseq_032802.*  
Database sequences: 747574  
Database length: 111073796  
Search time (sec): 193.710000
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seq\_documentation\_block:

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XX AAW70379;

DT 18-NOV-1998 (first entry)

XX Anti-human CD23 5E8 monoclonal antibody light chain variable region.

XX Anti-human CD23 5E8 monoclonal antibody; light chain variable region;

KW human CD23; IgE; FcεRI/CD23; gamma-1 constant region;

KW gamma-3 constant region; allergy; inflammation; autoimmune disease;

KW allergic rhinitis; conjunctivitis; autoimmune haemolytic anaemia.

OS Macaca fascicularis

XX Key Location/Qualifiers

FT Protein 1..22

FT Protein /note= "signal peptide"

FT Protein 23..129

FT Protein /note= "anti-human CD23 5E8 light chain variable

FT Binding-site 46..56

FT Binding-site /note= "CDR 1"

FT Binding-site 72..77

FT Binding-site /note= "CDR 2"

FT Binding-site 111..119

FT Binding-site /note= "CDR 3"

PN W09837099-A1.

XX 27-AUG-1998. 98WO-US02253.

XX 17-FEB-1998; 98US-0803085.

XX 05-FEB-1998; 98US-0803085.

XX 20-FEB-1997; 97US-0803085.

PA (IDEC-) IDEC PHARM CORP.

PA (SEKG ) SEIKAGAKU CORP.

XX Klotzer WS, Nakamura T, Reff ME;

XX WPI; 1998-467495/40.

XX N-PSDB; AAV33309.

XX New anti-human CD23 monoclonal antibody - used for inhibiting IgE

XX expression to treat or prevent allergic, inflammatory and

XX auto-immune conditions

XX Example 1; Pages 106-108; 146pp: English.

XX The present sequence represents the light chain variable region of

XX primate monoclonal antibody anti-human CD23 5E8. The invention

XX provides primate monoclonal antibodies which specifically bind human

XX CD23, the low affinity receptor for IgE (FcεRI/CD23), and comprise

XX either of a human gamma-1 or human gamma-3 constant region that binds

XX to human Fc gamma receptors and inhibits IgE expression. The monoclonal

XX antibodies of the invention are claimed to be useful for inhibiting

XX induced IgE production for treating or preventing allergic, inflammatory

XX and autoimmune conditions e.g. allergic rhinitis conjunctivitis,

XX auto-immune haemolytic anaemia, etc.

XX Sequence 129 AA;

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  Quality: 668.00      Length: 129
  Ratio: 5.178         Gaps: 0
  Percent Similarity: 100.000  Percent Identity: 100.000

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    1 MetaspMetargValProAlaGlnLeuLeuGlyLeuLeuLeuLeuIrpLe 17
    51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCCATCTTCCCTGT 100
    17 uProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
    101 CTGCATCTGAGGGACAGAGTCACCATCAGTTCAGGGCAAGTCAGGAC 150
    34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnAsp 50
    151 ATTAGGTATTATTAAATTTGATATCAGCAGAAACCCAGGAAAGCTCTAA 200
    51 IleArgTyrTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
    201 GCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGT 250
    67 sLeuLeuIleTyrValAlaSerSerLeuGlnSerGlyValProSerArgp 84
    251 TCAGCGCATGTGATCGGACAGAGTTCATCTCAGCGTCAGCAGCGCTG 300
    84 heSerGlySerGlySerGlyThrGluPheThrLeuThrValSerSerLeu 100
    301 CAGCCTGAAGATTTGGGACTTTTACTGTCTACAGGTTTATAGTACCCC 350
    101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnValTyrSerThrPr 117
    351 TCGGACGTTCCGGCAGGGACCAAGGTGGAATCAAA 387
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  XX
  DT 16-AUG-2000 (first entry)
  XX
  XX Human IGFAM-10 immunoglobulin.
  XX
  XX Human; immunoglobulin; IGFAM-10; IGFAM; immune disorder; cancer;
  KW infection; inflammation; haematopolesis; AIDS; allergy.
  XX
  XX Homo sapiens.
  XX
  XX Key Location/Qualifiers
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  FT /label= signal_peptide
  FT Protein 23..237
  FT /label= IGFAM-10
  FT Domain 38..112
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  XX
  XX W0200029583-A2.
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  XX
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PD 25-MAY-2000.
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PF 19-NOV-1999; 99WO-US27566.
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PR 19-NOV-1998; 99US-0113635.
PR 22-DEC-1998; 98US-0113635.
PR 07-APR-1999; 99US-0128194.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lal P, Hillman JL, Yang J;
XX
DR WPI; 2000-387796/33.
DR N-PSDB; AAA27390.
XX
PT Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders
PT .
XX
PS Claim 1; Page 85-86; 105pp; English.
XX
CC The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-10. Its gene was isolated from a cDNA library of colon
CC tissue. It is expressed in reproductive, gastrointestinal and
CC cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia,
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
CC multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
CC systemic lupus erythematosus and ulcerative colitis), complications of
CC cancer, haemodialysis and extracorporeal circulation, trauma and
CC haematopoietic cancer (such as leukaemia) and infections caused by
CC bacteria, viruses, fungi or parasites.
XX
SQ Sequence 237 AA;

alignment_scores:
  Quality: 594.50      Length: 130
  Ratio: 4.833         Gaps: 1
  Percent Similarity: 94.615  Percent Identity: 90.000

alignment_block:
  US-09-019-441-3 x AAY96298  ..

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    1 ATGCACATGAGGTCCTCCGCTCAGCTCCTGGGGCTCCTCTGCTCTGGCT 50
    1 MetaspMetargValProAlaGlnLeuLeuGlyLeuLeuLeuLeuIrpLe 17
    51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCCATCTTCCCTGT 100
    17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeuS 34
    101 CTGCATCTGTAGGGACAGAGTCACCATCAGTTCAGGGCAAGTCAGGAC 150
    34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50
    151 ATTAGGTATTATTAAATTTGATATCAGCAGAAACCCAGGAAAGCTCTAA 200
    51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
    201 GCTCCTGATCTATGTCATCCAGTTTGCAAGTGGGGTCCCATCAAGGT 250
    67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
    251 TCAGCGCATGTGATCGGACAGAGTTCATCTCAGCGTCAGCAGCGCTG 300
    117 oArgThrPheGlyGlnGlyThrLysValGluIleLys 129
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84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117  
351 TCGG...ACGTTCCGCCAAGGACCAAGTGGAAATCAAA 387  
117 oProIleThrPheGlyGlnGlyThrArgLeuGluIleLys 130

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.AAW22842

seq\_documentation\_block:  
ID AAW22842 standard; Protein; 132 AA.

XX AC AAW22842;

XX DT 12-SEP-1997 (first entry)

XX DE Human anti-tumour antigen antibody light chain variable region.

XX KW Human; tumour antigen; cancer; monoclonal; antibody; light chain;  
KW variable region; medicine; pharmacology; biochemistry; CDR;  
KW complementarity determining region.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= sig\_peptide  
FT Peptide 23..132  
FT /label= mat\_peptide  
FT Region 46..56  
FT /label= CDR\_1  
FT Region 72..78  
FT /label= CDR\_2  
FT Region 111..119  
FT /label= CDR\_3

XX JP09100300-A.

XX PD 15-APR-1997.

XX PF 03-OCT-1995; 95JP-0278266.

XX PR 03-OCT-1995; 95JP-0278266.

XX PA (HAGI/) HAGIWARA Y.

XX DR WPI: 1997-276726/25.

XX DR N-PSDB; AAT75423.

XX PT Anticancer human monoclonal antibody variable region sequences - and  
PT related DNA and RNA

XX PS Claim 9; Page 11; 14pp; Japanese.

XX CC The present sequence is a human anti-tumour antigen  
CC monoclonal antibody (MAB) light chain variable region, useful in  
CC medicine, pharmacology and biochemistry. The isotype of a MAB  
CC secreted by the human/human hybridoma HT was determined to be mu  
CC and kappa. Human MAB was purified, and the antigen recognised by  
CC human MAB CLN-IgM identified by western blotting.

XX SQ Sequence 132 AA;

alignment\_scores:

Quality: 592.00 Length: 129  
Ratio: 4.813 Gaps: 0  
Percent Similarity: 95.349 Percent Identity: 89.147

alignment\_block:

US-09-019-441-3 x AAW22842

Align seg 1/1 to: AAW22842 from: 1 to: 132

1 ATGCACATGAGGTCGCCGCTCAGCTCCTGGGCTCCTCTGTCTGGCT 50  
1 MetaspMetGluAlaHisValGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17  
51 CCAGGTGCCAGATGTGCATCCAGATGACCCAGTCTCCATCTTCCCTGT 100  
17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeu 34  
101 CTGCATCTAGGGGACAGAGTCCACATCCTTCAGGGCAAGTCAGGAC 150  
34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnSer 50  
151 ATTAGGTATTATTAAATTTGGTATCAGCAGAAACAGGAAAAGCTCCTAA 200  
51 IleSerSerTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GTCCTCATCTATGTTGCATCCAGTTCGAAAGTGGGGTCCCATCAAGGT 250  
67 sLeuLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84  
251 TCAGCGGCTGAGTCTGGGACAGAGTCTCCTCAGCGTCAGCGCTG 300  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTGGCACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnSerTyrSerThrPr 117  
351 TCGGACCTTCGCCAAGGACCAAGTGGAAATCAAA 387  
117 oGlnThrPheGlyGlnGlyThrLysValGluIleLys 129

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.AAY96289

seq\_documentation\_block:

ID AAY96289 standard; protein; 237 AA.

XX AC AAY96289;

XX DT 16-AUG-2000 (first entry)

XX DE Human IGFAM-1 immunoglobulin.

XX KW Human; immunoglobulin; IGFAM-1; IGFAM; immune disorder; cancer;  
XX infection; inflammation; haematopoiesis; AIDS; allergy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers  
FT Peptide 1..22  
FT /label= signal\_peptide  
FT Protein 23..237  
FT /label= IGFAM-1  
FT Domain 38..112  
FT /label= Ig\_domain  
FT Domain 150..219  
FT /label= Ig\_domain  
FT Region 154..176  
FT /label= Ig\_signature  
FT Domain 193..236  
FT /label= Ig\_domain  
FT Region 215..232  
FT /label= Ig\_signature

XX WO200029583-A2.

XX PD 25-MAY-2000.

XX PF 19-NOV-1999; 99WO-US27566.



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:|||||
17 eProGlyAlaArgCysAspIleGlnMetThrGlnSerProSerLeuS 34
101 CTCATCTGTAGGGGACAGAGTCCACCATCTTGCAGGGCAAGTCAGGAC 150
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34 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50
151 ATTAGGTATTATTAAATGGTATCAGCAGAAACACAGGAAAGCTCCTAA 200
|||||
51 IleArgAsnAspLeuGlyTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCCTGATCTATGTTCATCCAGTTCGAAAGTGGGTCCTCCATCAAGT 250
|||||
67 sArgLeuIleTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgp 84
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTG 300
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301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCC 350
|||||
101 GlnProGluAspPheAlaThrTyrTyrCysLeuGlnHisAsnSerAsnPr 117
351 TCGGAGCTTCGGCAAGGACCAAGGTGGAAATCAAA 387
|||||
117 oLeuThrPheGlyGlyThrLysValGluIleLys 129

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seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT:AA57482

seq\_documentation\_block:

ID AAR57482 standard; Protein; 129 AA.

AC AAR57482;

XX 02-OCT-1995 (first entry)

DE Humanized 1308F VL.

XX Monoclonal antibody; Mab; respiratory syncytial virus; RSV;  
 KW chimeric antibody; humanized antibody; antibody engineering;  
 KW light chain; VL; complementarity determining region; CDR.

XX Synthetic.

XX Key Location/Qualifiers

FT Region 46..54

FT /label= CDR1

FT Region 72..78

FT /label= CDR2

FT Region 111..119

FT /label= CDR3

XX W09417105-A.

XX 04-AUG-1994.

XX 29-JAN-1993; 93WO-US01168.

XX 29-JAN-1993; 93AU-0036608.

XX 29-JAN-1993; 93WO-US01168.

XX (MEDI-) MEDIMUNE INC.

XX Johnson L;

XX WPI; 1994-264037/32.

XX N-PSDB; AAQ67194.

XX Human-murine chimeric antibodies against respiratory syncytial

PT virus - comprises at least 1 CDR from each variable heavy and

PT light chain of at least 1 murine monoclonal antibody

PS Disclosure; Fig. 4A-4B; 34pp; English.

XX Synthetic overlapping oligonucleotides and the 5' primer given in  
 CC AAQ67197 and 3' primer of AAQ67198 were used to construct a DNA  
 CC sequence (AAQ67194) encoding humanized 1308F VL (AAR57482) in which  
 CC CDRs of the anti-RSV F antigen murine Mab 1308F VL region were  
 CC substituted into the homologous human K102 gene. Similar  
 CC procedures were used to obtain humanized 1308F VH for the  
 CC construction of anti-RSV F protein humanized antibody.  
 XX  
 SQ Sequence 129 AA;

alignment\_scores:  
 Quality: 577.00 Length: 129  
 Ratio: 4.769 Gaps: 0  
 Percent Similarity: 93.798 Percent Identity: 85.271

alignment\_block:

US-09-019-441-3 x AAR57482 ..

Align seg 1/1 to: AAR57482 from: 1 to: 129

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1 ATGCACATGAGGTCCTCCCGCTCAGCTCTGGGCTCTCTCTGCTCTGGCT 50
|||||
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 17
51 CCAGGTGGCAGATGTGACATCCAGATGACCCAGTCTCCATCTCCCTGT 100
|||||
17 uProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34
101 CTCATCTGTAGGGACAGAGTCCACCATCTTGCAGGGCAAGTCAGGAC 150
|||||
34 erAlaSerValGlyAspArgValThrIleThrCysLysAlaSerGlnasp 50
151 ATTAGGTATTATTAAATGGTATCAGCAGAAACACAGGAAAGCTCCTAA 200
|||||
51 IleAsnArgTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
201 GCTCCTGATCTATGTTCATCCAGTTCGAAAGTGGGTCCTCCATCAAGT 250
|||||
67 sLeuLeuIleTyrArgAlaAsnArgLeuValAspGlyValProSerArgp 84
251 TCAGCGCAGTGGATCTGGGACAGAGTTCACCTCTCACCGTCAGCAGCTG 300
|||||
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100
301 CAGCCTGAAGATTTGGGACTTATTACTGTCTACAGGTTTATAGTACCC 350
|||||
101 GlnProAspAspPheAlaThrTyrTyrCysLeuGlnPheHisGluPhePr 117
351 TCGGAGCTTCGGCCACAGGACCAAGGTGGAAATCAAA 387
|||||
117 oTyrThrPheGlyGlyThrLysLeuGluIleLys 129

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seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AA592085

seq\_documentation\_block:

ID AAR92085 standard; Protein; 129 AA.

XX AAR92085;

XX 15-MAY-1996 (first entry)

XX Humanised antibody 1308 VL.

XX Humanised antibody; chimeric antibody; antibody engineering;

KW monoclonal antibody; Mab 1308F; respiratory syncytial virus; RSV;

KW light chain; complementarity determining region; CDR.

XX Synthetic.

XX Key

XX Region Location/Qualifiers

FT 46..55

```

FT      Region      /label= CDR1
FT      72..78
FT      /label= CDR2
FT      111..119
FT      /label= CDR3
XX
XX      WO9605229-A1.
XX
XX      22-FEB-1996.
XX
XX      09-AUG-1995; 95WO-US10053.
XX
XX      15-AUG-1994; 94US-0290592.
XX
XX      (MEDI-) MEDIMMUNE INC.
XX
XX      Johnson LS;
XX
XX      WPI; 1996-139646/14.
XX      N-PSDB; AAT16181.
XX
XX      New chimeric antibodies against respiratory syncytial virus -
XX      comprise human antibodies with CDR's from the variable heavy and
XX      light chains of a murine antibody
XX
XX      Example 2; Fig 4A-4B; 55pp; English.
XX
XX      A human-mouse chimeric antibody light chain has a human HV3 framework
XX      contg. complementarity determining regions (CDRs) from the variable
XX      light (VL) chain of murine monoclonal antibody (Mab) 1308F active
XX      against respiratory syncytial virus (RSV) glycoprotein F antigenic
XX      site C. DNA (AAT16181) coding for CDR-grafted VL-encoding region,
XX      Hu1308 VL (AAR92085), was synthesized using overlapping
XX      oligonucleotides. The construct was used with Hu1308 VH (see AAR92084)
XX      for prodn. in COS-1 transfectants of humanised antibody useful for
XX      treatment of RSV infection.
XX
XX      Sequence 129 AA;
XX
alignment_scores:
XX      Quality: 577.00      Length: 129
XX      Ratio: 4.769      Gaps: 0
XX      Percent Similarity: 93.798      Percent Identity: 85.271
XX
alignment_block:
XX      US-09-019-441-3 x AAR92085
XX
Align seg 1/1 to: AAR92085 from: 1 to: 129
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1 ATGGACATGAGGTGCCCGCTCAGCTCCTGGGCTCCTCTGCTGGCT 50
XX
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpLe 17
XX
51 CCCAGGTGCCAGATGTCACATCAGATGACCCAGTCTCCATCTCCCTGT 100
XX
17 uproGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeuS 34
XX
101 CTCATCTGTAGGGGACAGAGTACCATCCTTGCAGGGCAAGTCAGGAC 150
XX
34 erAlaSerValGlyAspArgValThrIleThrCysLysAlaSerGlnAsp 50
XX
151 ATTAGGTATTATTAATTTGGTATCAGCAGAAACAGGAAAGCTCTCTAA 200
XX
51 IleAsnArgTyrLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67
XX
201 GCTCCCTGATCTATGTCATCCAGTTTGCNAAGTGGGTCCTCCATCAAGT 250
XX
67 sLeuLeuIleTyrArgAlaAsnArgLeuValAspGlyValProSerArgp 84
XX
*251 TCAGCGCAGTGGTGGGACAGAGTTCACTCTCACCGTTCAGCAGCCTG 300
XX
84 heSerGlySerGlySerGlyThrGluPheThrLeuThrIleSerLeu 100

```

```

301 CAGCCTGAAGATTTTGGAGCTTATTACTGCTACAGGTTTATAGTACCCC 350
XX
101 GlnProaspaspPheAlaThrTyrTyrCysLeuGlnPheHisGluPhePr 117
XX
351 TCGGACGTTTCGGCAGGAGGACAGGAGGTGGAAATCAAA 387
XX
117 oTyrThrPheGlyGlyThrLysLeuGluIleLys 129
XX
seq_name: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.AAY96301
seq_documentation_block:
ID AAY96301 standard; protein; 237 AA.
XX
AC AAY96301;
XX
DT 16-AUG-2000 (first entry)
XX
DE Human IGFAM-13 immunoglobulin.
XX
KW Human; immunoglobulin; IGFAM-13; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX
OS Homo sapiens.
XX
XX      Key      Location/Qualifiers
XX      FT      1..22
XX      FT      /label= signal_peptide
XX      FT      23..237
XX      FT      /label= IGFAM-13
XX      FT      38..112
XX      FT      /label= Ig_domain
XX      FT      150..219
XX      FT      /label= Ig_domain
XX      FT      193..236
XX      FT      /label= Ig_domain
XX
XX      WO200029583-A2.
XX
XX      25-MAY-2000.
XX
XX      19-NOV-1999; 99WO-US27566.
XX
XX      19-NOV-1998; 99US-0113635.
XX      22-DEC-1998; 98US-0113635.
XX      07-APR-1999; 99US-0128194.
XX
XX      (INCY-) INCYTE PHARM INC.
XX
XX      Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX      Lu DAM, Lal P, Hillman JL, Yang J;
XX
XX      WPI; 2000-387796/33.
XX      N-PSDB; AAA27393.
XX
XX      Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX      protein is useful for preventing and treating disorders associated with
XX      altered levels of the protein such as cancer, immune system disorders
XX
XX      Claim 1; Page 87-88; 105pp; English.
XX
XX      The present sequence is the human immunoglobulin superfamily protein
XX      IGFAM-13. Its gene was isolated from a cDNA library of lung tumour
XX      tissue. It is expressed in reproductive, gastrointestinal and
XX      cardiovascular tissue, where cancer and inflammation are common. The
XX      gene, protein, its antibodies, agonists and antagonists are suitable for
XX      diagnosing and treating many diseases, including cancer, immune system
XX      disorders (such as inflammation, AIDS, allergies, anaemia,
XX      arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's
XX      disease, diabetes mellitus, emphysema, Graves' disease, hepatitis,
XX      multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX      systemic lupus erythematosus and ulcerative colitis), complications of

```





117 nTyrAsnAspTyrProTrpThrPheGlyGlnGlyThrLysValGluIleL 134  
 386 AA 387  
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 134 ys 134

seq\_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT:AAV56737

seq\_documentation\_block:

ID AAY56737 standard; protein; 130 AA.

XX

AC

XX

DT

XX 15-FEB-2000 (first entry)

XX

DE

XX Amino acid sequence of Cynomolgous V kappa cDNA clone 4-10.

XX

KW Complementarity determining region; antibody; primate; immunogenicity;

XX Old World ape; Old World monkey; antigen-binding affinity.

XX

OS Macaca cynomolgus.

XX

PN WO9955369-A1.

XX

PD

XX 04-NOV-1999.

XX

PF 28-APR-1999; 99WO-US09131.

XX

PR 28-APR-1998; 98US-0083367.

XX

PA (SMIK ) SMITHKLINE BEECHAM CORP.

XX

PI Taylor AH;

XX

XX

DR WPI; 2000-023265/02.

XX

DR N-PSDB; AA29340.

XX

XX

XX

PT Antibodies containing donor complementarity determining regions and

XX non-human primate acceptor frameworks, having reduced immunogenicity in

XX humans -

XX

PS Example 4; Page 96-97; 123pp; English.

XX

CC The invention provides an antibody (Ab) comprising donor CDRs

XX (complementarity determining regions) derived from a non-human antigen-

CC specific donor antibody, and an acceptor framework from a non-human

XX primate. The Abs are prepared by grafting CDRs from a non-human antigen-

CC specific donor antibody onto homologous Old World ape or monkey acceptor

XX frameworks. The Abs have reduced immunogenicity and are better tolerated

CC in humans (because of the close similarity between the human and primate

XX proteins), but retain the full antigen-binding affinity of the donor

XX antibody.

XX

SQ Sequence 130 AA;

alignment\_scores:

Quality: 563.00

Ratio: 4.771

Percent Similarity: 91.473

Percent Identity: 86.047

alignment\_block:

US-09-019-441-3 x AAY56737 ..

Align seg 1/1 to: AAY56737 from: 1 to: 130

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1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuIle 17

|||||

51 CCCAGGTGCCAGATGTGACATCCAGATGACCCAGCTCTCCATCTTCCCTGT 100

|||||

17 uLeuGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeus 34

101 CTCATCTCTAGGGGACAGAGTCACCATCTTGCAGGGCAAGTCAGGAC 150  
 |||  
 34 erAlaSerValGlyAspArgValThrIleThrCysGlnAlaSerGlnGly 50  
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 151 ATTAGGTATTATTAAATTGGTATCAGCAGAACACAGGAAAGCTCTCTAA 200  
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 51 IleSerAsnTrpLeuAlaIleThrGlnGlnLysProGlyLysAlaProLy 67  
 |||  
 201 GCTCCTGATCTATGTTCATCCAGTTTGCAGTGGGGTCCCATCAAGT 250  
 |||  
 67 sLeuLeuIleTyrAlaAlaSerThrPheGlnSerGlyValProSerArgP 84  
 |||  
 251 TCACGGCAGTGTGATCGGACAGAGTCTCTACCTCACCCTCAGCAGCCTG 300  
 |||  
 84 heserGlySerGlySerGlyThrGluPheThrLeuThrIleSerSerLeu 100  
 |||  
 301 CACCGCTGAAGATTTGCGACTTATTACTGTCTACAGGTTTATAGTACCCC 350  
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 101 GlnProGluAspPheAlaThrTyrTyrCysGlnGlnThrAsnThrTyrPr 117  
 |||  
 351 TCGGACGTTTCGGCCAAAGGGACCAAGGTGGAAATCAAA 387  
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seq\_name: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT:AA77614

seq\_documentation\_block:

ID AAR77614 standard; Protein; 236 AA.

XX

AC AAR77614;

XX

DT 15-MAR-1996 (first entry)

XX

DE Humanised 5G1.1 VL + 012.

XX

XX

KW Complement C5; haemolysis; kidney; glomerulonephritis;

XX monoclonal antibody; antiinflammatory; antibody engineering;

XX humanised antibody; complementarity determining region; CDR;

XX ds.

XX

OS Synthetic.

XX

FH Key

XX Location/Qualifiers

FT Peptide

XX /label= sig\_peptide

FT Peptide

XX /label= mat\_peptide

FT Region

XX /label= CDR-L1

FT Region

XX /label= CDR-L2

FT Region

XX /label= CDR-L3

XX

PN WO9529697-A1.

XX

PD 09-NOV-1995.

XX

PF 01-MAY-1995; 95WO-US05688.

XX

PR 02-MAY-1994; 94US-0236208.

XX

XX (ALEX-) ALEXION PHARM INC.

XX

PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

XX Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

XX

DR WPI; 1995-392923/50.

XX

DR N-PSDB; AAT08486.

XX

PT Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis  
PS Claim 40; Page 132-34; 181pp; English.

XX A humanised CDR-grafted light chain, designated 5G1.1 VL + 012  
CC (AAR77614), includes CDRs derived from mouse anti-C5 monoclonal  
CC antibody 5G1.1. DNA (AAT08486) coding for the light chain can be  
CC subcloned together with DNA (AAT08484) coding for a humanised Fd  
CC (AAR77611) into vector APEX-3P (AAT08476) for expression of humanised  
CC antibody in human 293 EBNA cells. Such recombinant antibodies retain  
CC the ability of MAb 5G1.1 to block human complement C5a generation and  
CC thus to reduce glomerular inflammation and kidney dysfunction  
CC associated with glomerulonephritis.

XX Sequence 236 AA;

alignment\_scores:  
Quality: 562.00 Length: 129  
Ratio: 4.723 Gaps: 0  
Percent Similarity: 92.248 Percent Identity: 85.271

alignment\_block:  
US-09-019-441-3 x AAR77614

Align seg 1/1 to: AAR77614 from: 1 to: 236

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51 CCCAGGTGCCAGATGTGACATCCAGATCCAGATCCAGATCTCCATCTTCCCTGT 100  
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17 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeus 34  
101 CTGCATCTGTAGGGAGCAGATGACCATCACTTCAGGGGCAAGTCAGGAC 150  
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34 erAlaSerValGlyAspArgValThrIleThrCysGlyAlaSerGluasn 50  
151 ATTAGGTATTATTAAATGGTATCAGCAGAAACCCAGAAAGTCCCTAA 200  
|||||  
51 IleTyrGlyAlaLeuAsnTrpTyrGlnGlnLysProGlyLysAlaProLy 67  
201 GCCTCTGATCTATGTCATCCAGTTGCAAGTGGGGTCCCATCAAGGT 250  
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67 sLeuLeuIleTyrGlyAlaThrAsnLeuAlaAspGlyValProSerArgp 84  
251 TCAGCGCAGTGGATCGGACAGAGTTCACTCTCACAGTTTATAGTACCC 300  
|||||  
84 heSerGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTCGCACTTATTACTGTCTACAGTTTATAGTACCC 350  
|||||  
101 GlnProGluAspPheAlaThrTyrTyrCysGlnAsnValLeuAsnThrPr 117  
351 TCGGAGTTCGGCAGGGACCAAGGTGGAATCAAA 387  
|||||  
117 oLeuThrPheGlyGlnGlyThrLysValGluIleLys 129

seq\_name: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT:AAW03725

seq\_documentation\_block:

ID AAW03725 standard; Protein; 171 AA.  
XX AAW03725;  
AC  
XX  
XX  
DT 02-APR-1997 (first entry)  
XX  
XX Humanised MAb 39-1.106 light chain variable region.  
DE  
XX light chain; variable region; murine; mouse; anti-human; disease;  
KW glycoprotein 39; gp39; monoclonal; antibody; 39-1.106; hybridoma;  
KW diagnosis; inhibition; B-cell; activation; treatment; disorder;

KW immune; autoimmune; allergic response; organ rejection; drug;  
KW graft versus host; cell imaging; tumour; targeted; delivery;  
KW targeted; humanised.  
XX  
XX Mus musculus.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 2 /note= "corresponding codon TAG"  
FT Misc-difference 11 /note= "corresponding codon TAA"  
FT Misc-difference 157 /note= "corresponding codon TAA"  
FT Misc-difference 165 /note= "corresponding codon TAA"  
FT /note= "corresponding codon TAA"  
XX  
XX WO9623071-A2.  
XX  
XX 01-AUG-1996.  
XX  
XX 26-JAN-1996; 96WO-US01119.  
XX  
XX 26-JAN-1995; 95US-0379057.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Aruffo AA, Bajorath J, Gilliland LK, Gordon ML;  
XX Harris LJ, Hollenbaugh D, Siadak AW;  
XX WPI: 1996-362694/36.  
XX N-PSDB; AAT36018.  
XX  
XX Monoclonal antibodies specific for different epitope(s) on human  
XX gp39 - used for inhibiting B cell activation and for the diagnosis  
XX of various disorders, e.g. cancer, psoriasis etc..  
XX  
XX Example 13; Fig 16; 167pp; English.  
XX  
XX The present sequence is the light chain variable region of the  
XX humanised murine anti-human glycoprotein (gp) 39 monoclonal  
XX antibody (MAB) 39-1.106. The MAB may be useful for diagnosing  
XX disease states, inhibiting B-cell activation and for treating  
XX immunological disorders, e.g. autoimmune disorders, allergic  
XX responses, organ rejection and graft versus host disease. It may  
XX also be used for imaging cells which express gp39 on their surface,  
XX e.g. tumour cells, and to target therapeutic agents to such cells.  
XX The MAB inhibits the CD40/gp39 interaction, therefore limiting both  
XX prim. and sec. responses to T-cell dependent antigens and AB prodn.  
XX specific to these antigens. A typical compsn. for intramuscular  
XX injection pref. contains 50 mg of MAB in 1 ml of sterile buffered  
XX water.  
XX  
XX Sequence 171 AA;

alignment\_scores:  
Quality: 557.00 Length: 129  
Ratio: 4.720 Gaps: 0  
Percent Similarity: 91.473 Percent Identity: 83.721  
alignment\_block:  
US-09-019-441-3 x AAW03725  
Align seg 1/1 to: AAW03725 from: 1 to: 171  
1 ATGGACATGAGGTCCTCCGCTCAGCTCCTGGGCTCCTTCTGCTCTGGCT 50  
:::|||||  
21 IleAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuTrpLe 37  
51 CCCAGGTGCCAGATGTGACATCCAGATCCAGATCCAGTCTCCATCTTCCCTGT 100  
|  
37 uArgGlyAlaArgCysAspIleGlnMetThrGlnSerProSerSerLeus 54



101 CTGCATCTGTAGGGACAGAGTCCACCATCTTCAGGGCAAGTCAGGAC 150  
|||||  
54 erAlaSerValGlyAspArgValThrIleThrCysArgAlaSerGluThr 70  
|||||  
151 ATTAGGTATTATTAAATGGTATCATCAGCAAGAACAGGAAAGCTCCTAA 200  
|||||  
71 IleTyrSerTyrLeuAlaThrTyrGlnGlnLysProGlyLysAlaProLy 87  
|||||  
201 GTCCTCATCTATGTTGCATCCAGTTTGCAGGTTGAGGGGTCCTCAAGGT 250  
|||||  
87 sLeuLeuValTyrAsnAlaLysThrLeuAlaGluGlyValProSerArgp 104  
|||||  
251 TCAGCGCAGTGGATCTGGACAGAGTCTCCTCAGGTTTATAGTACCCC 300  
|||||  
104 heserGlySerGlySerGlyThrAspPheThrLeuThrIleSerSerLeu 120  
|||||  
301 CAGCCTGAAGATTTTGGCAGTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
121 GlnProGluAspPheAlaThrTyrTyrCysGlnHisHisTyrAsnThrPr 137  
|||||  
351 TCGGACGTTTCGGCCAGGGACCAAGTGGGAATCAAA 387  
|||||  
137 oLeuThrPheGlyGlyThrLysValGluIleLys 149

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA2000.DAT:AAV56721

seq\_documentation\_block:  
ID AAY56721 standard; protein; 129 AA.  
XX  
AC AAY56721;  
XX  
DT 15-FEB-2000 (first entry)  
XX  
DE Amino acid sequence of chimpanzee V kappa cDNA clone 46-7.  
XX  
KW Complementarity determining region; antibody; primate; immunogenicity;  
KW Old world ape; Old world monkey; antigen-binding affinity.  
XX  
OS Pan troglodytes.  
XX  
PN WO955369-Al.  
XX  
PD 04-NOV-1999.  
XX  
PF 28-APR-1999; 99WO-US09131.  
XX  
PR 28-APR-1999; 98US-0083367.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
XX  
PI Taylor AH;  
XX  
DR WPI: 2000-023265/02.  
DR N-PSDB; AAZ39324.  
XX

Antibodies containing donor complementarity determining regions and non-human primate acceptor frameworks, having reduced immunogenicity in humans -  
XX  
PS Example 2; Page 63-64; 123pp; English.  
XX  
CC The invention provides an antibody (Ab) comprising donor CDRs (complementarity determining regions) derived from a non-human antigen-specific donor antibody, and an acceptor framework from a non-human primate. The Abs are prepared by grafting CDRs from a non-human antigen-specific donor antibody onto homologous Old world ape or monkey acceptor frameworks. The Abs have reduced immunogenicity and are better tolerated in humans (because of the close similarity between the human and primate proteins), but retain the full antigen-binding affinity of the donor antibody.  
XX  
SQ Sequence 129 AA;

alignment\_scores:  
Quality: 556.00 Length: 129  
Ratio: 4.712 Gaps: 0  
Percent Similarity: 91.473 Percent Identity: 81.395  
alignment\_block:  
US-09-019-441-3 x AAY56721 ..  
Align seg 1/1 to: AAY56721 from: 1 to: 129  
1 ATGCATAGAGGTGCCCGCTCAGCTCCTGGGGTCTCTGCTGCTGGCT 50  
|||||  
1 MetAspMetArgValProAlaGlnLeuLeuGlyLeuLeuLeuLeuTrpPh 17  
51 CCAGGTGCCAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCCTGT 100  
|||||  
17 eProGlyAlaLysCysAspIleGlnMetThrGlnSerProSerThrLeu 34  
101 CTGCATCTGTAGGGACAGAGTCCACCATCTTCAGGGCAAGTCAGGAC 150  
|||||  
34 erAlaSerIleGlyAspArgValThrIleThrCysArgAlaSerGlnGly 50  
151 ATTAGGTATTATTAAATGGTATCATCAGCAAGAACAGGAAAGCTCCTAA 200  
|||||  
51 IleTyrAsnTyrLeuAsnThrTyrGlnGlnLysProGlyArgAlaProGl 67  
201 GTCCTCATCTATGTTGCATCCAGTTTGCAGGTTTATAGTACCCC 250  
|||||  
67 yLeuLeuIlePheGlyAlaArgAsnLeuGluThrGlyValProSerThrP 84  
251 TCAGCGCAGTGGATCTGGACAGAGTCTCCTCAGGTTTATAGTACCCC 300  
|||||  
84 heserGlySerGlySerGlyThrHisPheThrLeuThrIleSerSerLeu 100  
301 CAGCCTGAAGATTTTGGCAGTATTACTGTCTACAGGTTTATAGTACCCC 350  
|||||  
101 GlnProGlyAspPheAlaThrTyrTyrCysGlnGlnTyrTyrThrThrPr 117  
351 TCGGACGTTTCGGCCAGGGACCAAGTGGGAATCAAA 387  
117 oTyrThrPheGlyGlyThrLysLeuGluIleLys 129

seq\_name: /SIDS1/gcgdata/hold-geneseq/geneseq-embl/AA1993.DAT:AA838162

seq\_documentation\_block:  
ID AAR38162 standard; Protein; 234 AA.  
XX  
AC AAR38162;  
XX  
DT 01-OCT-1993 (first entry)  
XX

DE Sequence of the kappa light chain variable region (VK) of human immunoglobulin G3 (IgG3) produced by transformed human B-cell line 88BV59, ATCC CRL 10624.  
DE  
XX  
KW B-cell; immunoglobulin g; cancer; tumour.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Region  
FT 1..214  
FT /tag= a  
FT /label= 1st AA denoted AA#1  
FT 24..49  
FT /tag= b  
FT /label= CDR 1  
FT 50..88  
FT /tag= c  
FT /label= CDR 2  
FT 89..108  
FT /tag= d  
FT /label= CDR 3  
FT

FT Region 109..214  
FT /\*tag= e  
FT /label= CON  
XX  
XX EP546634-A.  
XX  
XX 16-JUN-1993.  
XX  
XX 09-DEC-1992; 92EP-0203827.  
XX  
XX 13-DEC-1991; 91US-0807300.  
XX  
XX (ALKU ) AKZO NV.  
XX  
XX Crichton VZ, Haspel MV, Kobrin BJ;  
XX  
XX WPI; 1993-190019/24.  
XX  
XX N-PSDB; AAQ43773.  
XX  
XX Transformed human B-cell line for monoclonal antibody prodn. for  
PT cancer diagnosis - prepd from peripheral blood B-cells of cancer  
PT patients actively immunised with autologous tumour antigen, for  
PT treating cancers  
XX  
XX Claim 9; Fig 3; 18pp; English.  
XX  
XX The 88BV59 kappa light chain sequence is indicated by the posns.  
CC of the CDRs and the constant region exon. 88BV59 utilises Vx1 and  
CC Jx5. The first NH2 terminal 22 residues were confirmed by AA  
CC sequencing.  
XX  
XX Sequence 234 AA;

alignment\_scores:  
Quality: 555.50 Length: 127  
Ratio: 4.748 Gaps: 1  
Percent Similarity: 92.126 Percent Identity: 86.614

alignment\_block:  
US-09-019-441-3 x AAR38162 ..

Align seg 1/1 to: AAR38162 from: 1 to: 234

10 AGGGTCCCGCTCAGCTCCGGGCTCCTCTGCTGGTCCAGGTGC 59  
||| |||||||||  
1 ArgGlyProAlaGlnLeuLeuGlyLeuLeuLeuTrpLeuProGlyAl 17  
60 CAGATGTGACATCCAGATGACCCAGTCTCCATCTTCCTGTCTGCATCTG 109  
||||| |||||||||  
17 aArgCysaspIleGlnLeuThrGlnSerProSerPheLeuSerAlaSerV 34  
110 TAGGGGACAGAGTCACCATCTTCAGGGCAAGTCAGGACATTAGGTAT 159  
||||| |||||||||  
34 aGlyAspArgValThrIleThrCysArgAlaSerGlnGlyIleSerSer 50  
160 TATTAAATTGGTATCAGCAGAAACAGAAAGCTCCTAAGCTCTCTGAT 209  
||||| |||||||||  
51 TyrLeuAlaTrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuII 67  
210 CTATGTTGCATCCAGTTTGCATAAGTGGGTCCCATCAAGGTTTCAGCGGCA 259  
||||| |||||||||  
67 eTyrAlaAlaSerSerLeuGlnSerGlyValProSerArgPheSerGlys 84  
260 GTGGATCTGGACAGAGTTTCACTCTCAGCTCAGCAGCCCTGCAGCCTGAA 309  
||||| |||||||||  
84 erGlySerGlyThrGluPheThrLeuThrIleSerSerLeuGlnProGlu 100  
310 GATTTTCGCACTTATTACTGTCTACAGGTTTATAGTACCCCTCGG...AC 356  
||||| |||||||||  
101 AspPheAlaThrTyrTyrCysGlnGlnLeuAsnGlyTyrProArgIleth 117  
357 GTTCGGCCCAAGGGACCAAGCTGGAAATCAAA 387

|||||  
117 rPheGlyGlnGlyThrArgLeuGluIleLys 127